

OM protein - protein search, using SW model
Run on: May 6, 2005, 17:11:07 ; Search time 16.8027 Seconds
Copyright (C) 1993 - 2005 Compugen Ltd.

RESULT 1
US-09-485-316A-11
Sequence 11, Application US/09485316A
Patient No. 6344441
GENERAL INFORMATION:
APPLICANT: Bihain, Bernard
APPLICANT: Bougueret, Lydie
APPLICANT: Yen-Potin, Frances
TITLE OF INVENTION: Lipoprotein-regulating medicaments
FILE REFERENCE: GENBET.036APC
CURRENT APPLICATION NUMBER: US/09/485,316A
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: FR 97/10088
PRIOR FILING DATE: 1997-08-06
PRIOR APPLICATION NUMBER: FR 98/05032
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: PCT IB98/01256
PRIOR FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent-PM
SEQ ID NO 11
LENGTH: 130
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: 1..130
OTHER INFORMATION: fragment 115..244 of translation from ref Genbank D45371
US-09-485-316A-11

Query Match 100.0%; Score 708; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 7.8e-80; Mismatches 0; Indels 0; Gaps 0;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSVQLETTVTPNMPIRPKTFKIPYQHNGDSTGKHCNTPOLYFYAHITYMVKVS 60
Dy 1 FSVQLETTVTPNMPIRPKTFKIPYQHNGDSTGKHCNTPOLYFYAHITYMVKVS 60

QY 61 LFKKDKAMFLFTYDQYQENNYDQASSVSLVLLHEVGDDWMLQYGEGERGLYADNDNSTP 120
Dy 61 LFKKDKAMFLFTYDQYQENNYDQASSVSLVLLHEVGDDWMLQYGEGERGLYADNDNSTP 120

QY 121 TGFELIYHDTN 130
Dy 121 TGFELIYHDTN 130

ALIGNMENTS

RESULT 2
US-09-530-423-2
Sequence 2, Application US/09530423
; Sequence 2, Application US/09530423

```

; Patent No. 6461821
; GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a
; TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit
; TITLE OF INVENTION: therefor
; FILE REFERENCE: P98-51
; CURRENT APPLICATION NUMBER: US/09/530,423
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: JP H9-297569
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO: 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Abdominal fat tissue from myoma uteri
; US-09-530-423-2

Query Match 100.0%; Score 708; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 1. 8e-79; Indels 0; Gaps 0;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PSVGLETTYVTPNMPIRFTKIFYNQNHQDGSTGKFCNIPGLYFAVHITVYMKDVKS 60
Db 102 PSVGLETTYVTPNMPIRFTKIFYNQNHQDGSTGKFCNIPGLYFAVHITVYMKDVKS 161
Qy 61 LFKKOKAMLFYDQOENNNDQASGSVLLHLEVGQWMLQVYGEGERGLYADNDNSTP 120
Db 162 LFKKOKAMLFYDQOENNNDQASGSVLLHLEVGQWMLQVYGEGERGLYADNDNSTP 221
Qy 121 TGFLLYHDTN 130
Db 222 TGFLLYHDTN 231

RESULT 3
US-08-463-911-7
; Sequence 7, Application US/084633911
; Patent No. 569330
; GENERAL INFORMATION:
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
; TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millett Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,911
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH195-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE: PatentIn Ver. 2.0
LENGTH: 244
TYPE: amino acid

; US-09-140-804-3
; ORGANISM: Homo sapiens
; TYPE: PRT
; US-09-140-804-3

Query Match 100.0%; Score 708; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 1. 9e-79; Indels 0; Gaps 0;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PSVGLETTYVTPNMPIRFTKIFYNQNHQDGSTGKFCNIPGLYFAVHITVYMKDVKS 60
Db 115 PSVGLETTYVTPNMPIRFTKIFYNQNHQDGSTGKFCNIPGLYFAVHITVYMKDVKS 174
Qy 61 LFKKOKAMLFYDQOENNNDQASGSVLLHLEVGQWMLQVYGEGERGLYADNDNSTP 120
Db 175 LFKKOKAMLFYDQOENNNDQASGSVLLHLEVGQWMLQVYGEGERGLYADNDNSTP 234

RESULT 5
US-09-336-536-20
; Sequence 20, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bosson, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 783-144
; CURRENT APPLICATION NUMBER: US/09/336,536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0

```

SEQ ID NO 20 ; PRINTER: PRT
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-09-336-536-20

Query Match 100.0%; Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-79; Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0; PRIMER: FSGVLETTVTIPNMPIRFTKIFNQNYTQHGDSTCKFHCMNIPGLYFAVHITVNMKDVKVS

QY 1 FSGVLETTVTIPNMPIRFTKIFNQNYTQHGDSTCKFHCMNIPGLYFAVHITVNMKDVKVS 60
Db 115 FSGVLETTVTIPNMPIRFTKIFNQNYTQHGDSTCKFHCMNIPGLYFAVHITVNMKDVKVS 174
QY 61 LFKKDCKAMLFPTYDQYQENNVDQASGSVLUHLEVGDDQWNLQVYGERGERGLYADNDNSTP 120
Db 175 LFKKDCKAMLFPTYDQYQENNVDQASGSVLUHLEVGDDQWNLQVYGERGERGLYADNDNSTP 234

QY 121 TGFLYHDTN 130
Db 235 TGFLYHDTN 244

RESULT 6 US-09-530-423-1

; Sequence 1, Application US/09530423
; Patent No. 6461821
; GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a kit
; TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit
; TITLE OF INVENTION: theretor
; FILE REFERENCE: P98-51
; CURRENT APPLICATION NUMBER: US/09/530,423
; CURRENT FILING DATE: 2000-05-01
; PRIORITY APPLICATION NUMBER: JP H9-237569
; PRIORITY FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Abdominal fat tissue from myoma uteri

Query Match 100.0%; Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-79; Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0; PRIMER: FSGVLETTVTIPNMPIRFTKIFNQNYTQHGDSTCKFHCMNIPGLYFAVHITVNMKDVKVS

QY 1 FSGVLETTVTIPNMPIRFTKIFNQNYTQHGDSTCKFHCMNIPGLYFAVHITVNMKDVKVS 60
Db 115 FSGVLETTVTIPNMPIRFTKIFNQNYTQHGDSTCKFHCMNIPGLYFAVHITVNMKDVKVS 174
QY 61 LFKKDCKAMLFPTYDQYQENNVDQASGSVLUHLEVGDDQWNLQVYGERGERGLYADNDNSTP 120
Db 175 LFKKDCKAMLFPTYDQYQENNVDQASGSVLUHLEVGDDQWNLQVYGERGERGLYADNDNSTP 234

QY 121 TGFLYHDTN 130
Db 235 TGFLYHDTN 244

RESULT 7 US-09-530-423-1

; Sequence 3, Application US/09686838B
; Patent No. 648612
; GENERAL INFORMATION:
; APPLICANT: Shappard, Paul O.
; APPLICANT: Holmes, Jacqueline M.
; TITLE OF INVENTION: Adipocyte-Specific Protein Homolog
; FILE REFERENCE: 97-491
; CURRENT APPLICATION NUMBER: US/09/686, 838B
; CURRENT FILING DATE: 2000-10-10

Query Match 100.0%; Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-79; Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0; PRIMER: FSGVLETTVTIPNMPIRFTKIFNQNYTQHGDSTCKFHCMNIPGLYFAVHITVNMKDVKVS

QY 1 FSGVLETTVTIPNMPIRFTKIFNQNYTQHGDSTCKFHCMNIPGLYFAVHITVNMKDVKVS 60
Db 115 FSGVLETTVTIPNMPIRFTKIFNQNYTQHGDSTCKFHCMNIPGLYFAVHITVNMKDVKVS 174
QY 61 LFKKDCKAMLFPTYDQYQENNVDQASGSVLUHLEVGDDQWNLQVYGERGERGLYADNDNSTP 120
Db 175 LFKKDCKAMLFPTYDQYQENNVDQASGSVLUHLEVGDDQWNLQVYGERGERGLYADNDNSTP 234

QY 121 TGFLYHDTN 130
Db 235 TGFLYHDTN 244

RESULT 9 US-09-686-838B-3

; Sequence 3, Application US/09552225A
; Patent No. 6521233

Query Match 100.0%; Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-79; Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0; PRIMER: FSGVLETTVTIPNMPIRFTKIFNQNYTQHGDSTCKFHCMNIPGLYFAVHITVNMKDVKVS

QY 1 FSGVLETTVTIPNMPIRFTKIFNQNYTQHGDSTCKFHCMNIPGLYFAVHITVNMKDVKVS 60
Db 115 FSGVLETTVTIPNMPIRFTKIFNQNYTQHGDSTCKFHCMNIPGLYFAVHITVNMKDVKVS 174
QY 61 LFKKDCKAMLFPTYDQYQENNVDQASGSVLUHLEVGDDQWNLQVYGERGERGLYADNDNSTP 120
Db 175 LFKKDCKAMLFPTYDQYQENNVDQASGSVLUHLEVGDDQWNLQVYGERGERGLYADNDNSTP 234

QY 121 TGFLYHDTN 130
Db 235 TGFLYHDTN 244

GENERAL INFORMATION:
 APPLICANT: Biddington, Christopher S.
 APPLICANT: Bishop, Paul
 TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACRP3
 FILE REFERENCE: 99-09
 CURRENT FILING DATE: 2000-04-19
 PRIOR APPLICATION NUMBER: 60/130,199
 PRIOR FILING DATE: 1999-04-20
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 3
 LENGTH: 244
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-552-225A-3

Query Match 100.0%: Score 708; DB 4; Length 244;
 Best Local Similarity 100.0%; Pred. No. 1.9e-79; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSVGLETTYVTPNMPIRPTKIFYNQONHYDGSTGKPHCNIPGLYPAHYTVMKDVKVS 60
 Db 115 PSVGLETTYVTPNMPIRPTKIFYNQONHYDGSTGKPHCNIPGLYPAHYTVMKDVKVS 174

Qy 61 LFKKOKAMLFYDQYQENNNDQASGSVLLHLEVGDQWMLQVYGERGNGLYADNDNSTF 120
 Db 175 LFKKOKAMLFYDQYQENNNDQASGSVLLHLEVGDQWMLQVYGERGNGLYADNDNSTF 234

Qy 121 TGFLLYHDTN 130
 Db 235 TGFLLYHDTN 244

RESULT 10
 US-09-619-740-51
 Sequence 51, Application US/09619740
 Patent No. 65544946
 GENERAL INFORMATION:
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Lasser, Gerald W.
 APPLICANT: Bishop, Paul D.
 TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION
 FILE REFERENCE: 99-12C3
 CURRENT APPLICATION NUMBER: US/09/619,740
 CURRENT FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: 09/253,604
 PRIOR FILING DATE: 1999-02-19
 PRIOR APPLICATION NUMBER: 09/444,794
 PRIOR FILING DATE: 1999-11-22
 PRIOR APPLICATION NUMBER: 09/506,855
 NUMBER OF SEQ ID NOS: 55
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO: 51
 LENGTH: 244
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-619-740-51

Query Match 100.0%: Score 708; DB 4; Length 244;
 Best Local Similarity 100.0%; Pred. No. 1.9e-79; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSVGLETTYVTPNMPIRPTKIFYNQONHYDGSTGKPHCNIPGLYPAHYTVMKDVKVS 60
 Db 115 PSVGLETTYVTPNMPIRPTKIFYNQONHYDGSTGKPHCNIPGLYPAHYTVMKDVKVS 174

Qy 61 LFKKOKAMLFYDQYQENNNDQASGSVLLHLEVGDQWMLQVYGERGNGLYADNDNSTF 120
 Db 175 LFKKOKAMLFYDQYQENNNDQASGSVLLHLEVGDQWMLQVYGERGNGLYADNDNSTF 234

Qy 121 TGFLLYHDTN 130
 Db 235 TGFLLYHDTN 244

RESULT 11
 US-09-776-976-6
 Sequence 6, Application US/09776976
 Patent No. 6566332
 GENERAL INFORMATION:
 APPLICANT: Fruebis, Joachim
 APPLICANT: Erickson, Mary Ruth
 APPLICANT: Yen, Frances
 APPLICANT: Bihain, Bernard
 TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
 CURRENT APPLICATION NUMBER: US/09/776,976
 CURRENT FILING DATE: 2001-02-05
 PRIOR APPLICATION NUMBER: US 09/58,055
 PRIOR FILING DATE: 2001-01-10
 PRIOR APPLICATION NUMBER: US 60/176,228
 PRIOR FILING DATE: 2000-01-14
 PRIOR APPLICATION NUMBER: US 60/198,087
 PRIOR FILING DATE: 2000-04-13
 PRIOR APPLICATION NUMBER: US 60/299,881
 PRIOR FILING DATE: 2000-09-01
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: Patent.pm
 SEQ ID NO: 6
 LENGTH: 244
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-776-976-6

Query Match 100.0%: Score 708; DB 4; Length 244;
 Best Local Similarity 100.0%; Pred. No. 1.9e-79; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSVGLETTYVTPNMPIRPTKIFYNQONHYDGSTGKPHCNIPGLYPAHYTVMKDVKVS 60
 Db 115 PSVGLETTYVTPNMPIRPTKIFYNQONHYDGSTGKPHCNIPGLYPAHYTVMKDVKVS 174

Qy 61 LFKKOKAMLFYDQYQENNNDQASGSVLLHLEVGDQWMLQVYGERGNGLYADNDNSTF 120
 Db 175 LFKKOKAMLFYDQYQENNNDQASGSVLLHLEVGDQWMLQVYGERGNGLYADNDNSTF 234

Qy 121 TGFLLYHDTN 130
 Db 235 TGFLLYHDTN 244

RESULT 12
 US-09-903-547-6
 Sequence 6, Application US/09903547
 Patent No. 6579852
 GENERAL INFORMATION:
 APPLICANT: Fruebis, Joachim
 APPLICANT: Erickson, Mary Ruth
 APPLICANT: Yen, Frances
 APPLICANT: Bihain, Bernard
 TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
 FILE REFERENCE: 76-US6.CIP
 CURRENT APPLICATION NUMBER: US/09/903,547
 CURRENT FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: US 09/776,976
 PRIOR FILING DATE: 2001-02-05
 PRIOR APPLICATION NUMBER: US 09/758,055
 PRIOR FILING DATE: 2001-01-10
 PRIOR APPLICATION NUMBER: US 60/299,881
 PRIOR FILING DATE: 2000-09-01
 PRIOR APPLICATION NUMBER: US 60/198,087
 PRIOR FILING DATE: 2000-04-13
 PRIOR APPLICATION NUMBER: US 60/176,228
 PRIOR FILING DATE: 2000-01-14

Qy 1 PSVGLETTYVTPNMPIRPTKIFYNQONHYDGSTGKPHCNIPGLYPAHYTVMKDVKVS 60
 Db 115 PSVGLETTYVTPNMPIRPTKIFYNQONHYDGSTGKPHCNIPGLYPAHYTVMKDVKVS 174

Qy 61 LFKKOKAMLFYDQYQENNNDQASGSVLLHLEVGDQWMLQVYGERGNGLYADNDNSTF 120
 Db 175 LFKKOKAMLFYDQYQENNNDQASGSVLLHLEVGDQWMLQVYGERGNGLYADNDNSTF 234

Qy 121 TGFLLYHDTN 130

Query Match 100.0%; Score 708; DB 4; Length 244;
 Best Local Similarity 100.0%; Pred. No. 1. 9e-79;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ORGANISM: Homo sapiens

US-09-909-547-6

Query Match 100.0%; Score 708; DB 4; Length 244;
 Best Local Similarity 100.0%; Pred. No. 1. 9e-79;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ORGANISM: Homo sapiens

QY 1 FSVGLEYTVTIPNMPIRFTKIFYNQHNDYDSTGKFCNCNIPGLYVFAYHITVYMKDVKS 60
 Db 115 FSVGLEYTVTIPNMPIRFTKIFYNQHNDYDSTGKFCNCNIPGLYVFAYHITVYMKDVKS 60
 QY 61 LFKKDKKAMLFYDQOENNYDQASGSVLLHLEVGDQWLOQYGEGERGLYADNDNSTP 120
 Db 175 LFKKDKKAMLFYDQOENNYDQASGSVLLHLEVGDQWLOQYGEGERGLYADNDNSTP 120
 QY 175 LFKKDKKAMLFYDQOENNYDQASGSVLLHLEVGDQWLOQYGEGERGLYADNDNSTP 234
 Db 121 TGFLLYHDTN 130
 QY 235 TGFLLYHDTN 244

RESULT 13
 US-09-569-852B-6
 Sequence 6, Application US/09569852B
 ; Parent No. 6582909
 ; GENERAL INFORMATION:
 ; APPLICANT: Bougueret, Lydie
 ; APPLICANT: Bihain, Bernard
 ; APPLICANT: Denison, Blake
 ; APPLICANT: Yen-Potin, France
 ; TITLE OF INVENTION: APML Biallelic Markers and Uses Thereof
 ; FILE REFERENCE: GEN-T113XC2
 ; CURRENT APPLICATION NUMBER: US/09/569, 852B
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: PCT/IB99/01858
 ; PRIOR FILING DATE: 1999-11-04
 ; PRIOR APPLICATION NUMBER: US 09/434, 848
 ; PRIOR FILING DATE: 1998-11-04
 ; PRIOR APPLICATION NUMBER: US 60/119, 593
 ; PRIOR FILING DATE: 1999-02-10
 ; PRIOR APPLICATION NUMBER: US 60/107, 113
 ; PRIOR FILING DATE: 1998-11-04
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 SEQ ID NO 6
 LENGTH: 244
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (15)..(15)
 OTHER INFORMATION: The 'xaa' at location 15 stands for GLY.
 NAME/KEY: misc_feature
 LOCATION: (1)..(367)
 OTHER INFORMATION: homology with 5' EST A254990 in private bank : GENSET
 LOCATION: (91)..(93)
 OTHER INFORMATION: Amino acid at position 15 (xaa) means GLY
 NAME/KEY: misc_feature
 LOCATION: (15)..(15)
 OTHER INFORMATION: The 'xaa' at location 15 stands for GLY.
 US-09-569-852B-6

Query Match 100.0%; Score 708; DB 4; Length 244;
 Best Local Similarity 100.0%; Pred. No. 1. 9e-79;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ORGANISM: Mus musculus

QY 1 FSVGLEYTVTIPNMPIRFTKIFYNQHNDYDSTGKFCNCNIPGLYVFAYHITVYMKDVKS 60
 Db 121 TGFLLYHDTN 130
 QY 235 TGFLLYHDTN 244

RESULT 14
 US-09-552-204A-3
 Sequence 3, Application US/09552204A
 ; Parent No. 6620909
 ; GENERAL INFORMATION:
 ; APPLICANT: Piddington, Christopher S.
 ; APPLICANT: Bishop, Paul D.
 ; APPLICANT: ADIPOCTE-SPECIFIC PROTEIN HOMOLOG ZACRP2
 ; FILE REFERENCE: 99-08
 ; CURRENT APPLICATION NUMBER: US/09/552, 204A
 ; CURRENT FILING DATE: 2000-04-19
 ; PRIOR APPLICATION NUMBER: 60/130, 207
 ; PRIOR FILING DATE: 1999-04-20
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 244
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-552-204A-3

Query Match 100.0%; Score 708; DB 4; Length 244;
 Best Local Similarity 100.0%; Pred. No. 1. 9e-79;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ORGANISM: Homo sapiens

QY 1 FSVGLEYTVTIPNMPIRFTKIFYNQHNDYDSTGKFCNCNIPGLYVFAYHITVYMKDVKS 60
 Db 115 FSVGLEYTVTIPNMPIRFTKIFYNQHNDYDSTGKFCNCNIPGLYVFAYHITVYMKDVKS 60
 QY 61 LFKKDKKAMLFYDQOENNYDQASGSVLLHLEVGDQWLOQYGEGERGLYADNDNSTP 120
 Db 175 LFKKDKKAMLFYDQOENNYDQASGSVLLHLEVGDQWLOQYGEGERGLYADNDNSTP 120
 QY 175 LFKKDKKAMLFYDQOENNYDQASGSVLLHLEVGDQWLOQYGEGERGLYADNDNSTP 234
 Db 121 TGFLLYHDTN 130
 QY 235 TGFLLYHDTN 244

RESULT 15
 US-09-485-316A-13
 Sequence 13, Application US/09485316A
 ; Parent No. 634441
 ; GENERAL INFORMATION:
 ; APPLICANT: Bihain, Bernard
 ; APPLICANT: Bougueret, Lydie
 ; APPLICANT: Yen-Potin, France
 ; TITLE OF INVENTION: Lipoprotein-regulating medicament
 ; FILE REFERENCE: GENSET_036APC
 ; CURRENT APPLICATION NUMBER: US/09/485, 316A
 ; CURRENT FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: FR 97/10088
 ; PRIOR FILING DATE: 1997-09-06
 ; PRIOR APPLICATION NUMBER: FR 98/05032
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: PCT IB98/01256
 ; PRIOR FILING DATE: 1998-08-06
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn
 ; LENGTH: 130
 ; TYPE: PRT
 ; ORGANISM: Mus musculus

US-09-485-316A-13

; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: 1..130
; OTHER INFORMATION: fragment 118..267 of translation from ref genbank U37222
US-09-485-316A-13

Query Match 92.5%; Score 655; DB 3; Length 130;
Best local Similarity 91.5%; Pred. No. 2.9e-73;
Matches 119; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 1 FSVGLRTTYVMPNMPIRFTKIFYQYNGHNGYQSTGKPHCNIFGLLYPAVHITVYMKDVKS 60
Db 1 FSVGLRTVTPNVPIRFTKIFYQYNGHNGYQSTGKPHCNIFGLLYPAVHITVYMKDVKS 60
QY 61 LPKKOKAMLYTYDQOENNTDQASSVLUHLEVGQWMLQVYGEGERGLYADNDSTP 120
Db 61 LPKKOKAVLFLTYDQOEKNTDQASGSVLUHLEVGQWMLQVYGDQWMLQVYGDQDNGLYADNDSTP 120
QY 121 TGFLLXHDTN 130
Db 121 TGFLLXHDTN 130

Search completed: May 6, 2005, 17:33:03
Job time : 17.8027 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: MAY 6, 2005, 17:05:01 ; Search time 77.0651 Seconds
(without alignments)
652.420 Million cell updates/sec

Title: US-10-072-159-11

Perfect score: 708
Sequence: 1 FSVGLETYVTIPNMPIRFTK..... YADNDNDSTFTGFLLYHDIN 130

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 2105692 seqs, 38676031 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*

1: geneseqD1990s:*

2: geneseqD1990s:*

3: geneseqD2008s:*

4: geneseqD2008s:*

5: geneseqD2008s:*

6: geneseqD2003bs:*

7: geneseqD2003bs:*

8: geneseqD2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	708	100.0	130 2 AY01485	Ay01485 Apml prot
2	708	100.0	130 7 ADE3609	Ade93609 Human adi
3	708	100.0	137 7 ADE3608	Ade93608 Human adi
4	708	100.0	144 7 ADE3607	Ade93607 Human adi
5	708	100.0	145 7 ADE3613	Ade93613 Human adi
6	708	100.0	157 7 ADE3606	Ade93606 Human adi
7	708	100.0	163 7 ADE3612	Ade93612 Human adi
8	708	100.0	163 7 ADE3615	Ade93615 Human adi
9	708	100.0	187 7 ADE3615	Ade93615 Human adi
10	708	100.0	193 7 ADE93614	Ade93614 Human adi
11	708	100.0	203 7 ADE3605	Ade93605 Human adi
12	708	100.0	226 7 ADE3604	Ade93604 Human adi
13	708	100.0	231 2 AY01808	Ay01808 Adipose m
14	708	100.0	231 4 AAB0347	Aab60347 Recombina
15	708	100.0	233 7 ADD3530	Add93530 Novel NOV
16	708	100.0	244 2 AY021807	Ay021807 Adipose m
17	708	100.0	244 3 AY071053	Ay071053 Human APm
18	708	100.0	244 3 AY071035	Ay071035 Human APm
19	708	100.0	244 3 AAB0323	Aab60323 Human adi
20	708	100.0	244 4 AAB05828	Aab65828 Human adi
21	708	100.0	244 4 AAB0529	Aae0529 Human OBG
22	708	100.0	244 4 AAB49598	Aab49598 Human ACr
23	708	100.0	244 4 AAB0373	Aab50373 Human adi
24	708	100.0	244 4 AAB49592	Aab49592 Human ACr
25	708	100.0	244 5 ABB08223	Abd08223 Human apm

ALIGNMENTS

RESULT 1	AY01485	ID AY01485 standard; peptide; 130 AA.
XX	XX	AC AY01485;
XX	XX	DT 21-MAY-1999 (first entry)
XX	XX	DE Apml protein fragment (residues 115-244).
XX	XX	KW Dietary lipid; liver; peripheral tissue; medicament; C1q complement; partitioning; lipolysis stimulated receptor; LSR; hypertension; gcgQ.R; obesity; atherosclerosis; insulin resistance; obesity-related disease; microangiopathy; Type II diabetes; ocular lesion; renal lesion; cachexia; neoplastic; eating disorder; Apml.
XX	XX	KW partitioning; lipolysis stimulated receptor; LSR; hypertension; gcgQ.R; obesity; atherosclerosis; insulin resistance; obesity-related disease; microangiopathy; Type II diabetes; ocular lesion; renal lesion; cachexia; neoplastic; eating disorder; Apml.
XX	XX	OS Homo sapiens.
XX	XX	PN WO9907736-A2.
XX	XX	PD
18-FEB-1999.	PF 06-AUG-1998:	998WO-1B001256.
XX	XX	06-AUG-1997; 97FR-00010088.
XX	XX	22-APR-1998; 98FR-00005032.
XX	XX	{GEST } GENSET. (INRNM) INSRM. INST NAT SANTE & RECH MEDICALE.
XX	XX	PI BIhain B, Bougueret L, Yen-Potin F;
XX	XX	DR WPI; 1999-157364/14.
XX	XX	PS
CC	CC	The invention relates to agents which influence the partitioning of dietary lipids between the liver and peripheral tissue for use as medicaments. Sequences shown in AY01481-488 that relate to C1q complements family and two consensus sequences (AY01499-500) are potentially useful as such agents. Compounds that influences the partitioning of dietary lipids between the liver and peripheral tissues can be used in medicament for treating a condition in which the partitioning of dietary lipids to the liver is abnormal. A polypeptide

XX 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001035.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
 XX PA (MAXY-) MAXYGEN HOLDINGS LTD.
 XX PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
 PT Bognes A;
 XX WPI; 2003-598262/56:
 PT New conjugate comprising an adiponectin polypeptide and a first non-
 PT polypeptide moiety, useful for preparing a composition for treating a
 PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
 XX Claim 14; SEQ ID NO 6; 184pp; English.
 XX CC The invention relates to a novel conjugate comprising an adiponectin
 CC polypeptide and a first non-polypeptide moiety covalently attached to the
 CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
 CC acid residue having an attachment group for the first non-polypeptide
 CC moiety which has been introduced in a position where the parent
 CC adiponectin is occupied by a surface exposed amino acid residue. The
 CC conjugate of the invention demonstrates antiatherosclerotic, antidiabetic,
 CC dermatological, immunosuppressive, immunomodulator and anorectic
 CC activities and may be useful for treating diabetes, obesity, atherosclerosis,
 CC cardiovascular diseases, dyslipidemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC current sequence is that of the human adiponectin apm1 protein of the
 CC invention.
 XX SQ Sequence 137 AA:
 Query Match 100.0%; Score 708; DB 7; Length 137;
 Best Local Similarity 100.0%; Pred. No. 3.8e-78;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FSVGLEYTVTIPNMPIRTKIFYNQHNYDGSTGKFCNPIGLYFAHYITVYMKDVKVS 60
 Db 8 FSVGLEYTVTIPNMPIRTKIFYNQHNYDGSTGKFCNPIGLYFAHYITVYMKDVKVS 67
 Qy 61 LFKKKDKAMLFYDQYQENNDQASGSVVLHLEVGDDQWLNQVYGEGERGLYADNDNSTF 120
 Db 68 LFKKKDKAMLFYDQYQENNDQASGSVVLHLEVGDDQWLNQVYGEGERGLYADNDNSTF 127
 Qy 121 TGFLLYHDTN 130
 Db 128 TGFLLYHDTN 137
 XX SQ Sequence 144 AA:
 Query Match 100.0%; Score 708; DB 7; length 144;
 Best Local Similarity 100.0%; Pred. No. 4.1e-78;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FSVGLEYTVTIPNMPIRTKIFYNQHNYDGSTGKFCNPIGLYFAHYITVYMKDVKVS 60
 Db 15 FSVGLEYTVTIPNMPIRTKIFYNQHNYDGSTGKFCNPIGLYFAHYITVYMKDVKVS 74
 Qy 61 LFKKKDKAMLFYDQYQENNDQASGSVVLHLEVGDDQWLNQVYGEGERGLYADNDNSTF 120
 Db 75 LFKKKDKAMLFYDQYQENNDQASGSVVLHLEVGDDQWLNQVYGEGERGLYADNDNSTF 134
 Qy 121 TGFLLYHDTN 130
 Db 135 TGFLLYHDTN 144
 RESULT 4
 ADE93607 standard; protein: 144 AA.
 ID ADE93607
 XX AC ADE93607;
 XX DT 12-FEB-2004 (first entry)
 XX DE Human adiponectin apm1(101-244) protein.
 XX KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
 KW antirheumatic; antibacterial; antilipaemic; dermatological;

KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 KW atherosclerosis; cardiovascular disease; dyslipidaemia;
 KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 KW myocardial infarction; inflammation; gene therapy; human; apm1;
 KW wild-type.
 XX OS Homo sapiens.
 XX PN WO2003055916-A2.
 XX PD 10-JUL-2003.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001US-0343482P.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
 XX PA (MAXY-) MAXYGEN HOLDINGS LTD.
 XX PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
 PT Bognes A;
 XX WPI; 2003-598262/56:
 PT New conjugate comprising an adiponectin polypeptide and a first non-
 PT polypeptide moiety, useful for preparing a composition for treating a
 PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
 XX Claim 44; SEQ ID NO 5; 184pp; English.
 XX CC The invention relates to a novel conjugate comprising an adiponectin
 CC polypeptide and a first non-polypeptide moiety covalently attached to the
 CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
 CC acid residue having an attachment group for the first non-polypeptide
 CC moiety which has been introduced in a position where the parent
 CC adiponectin is occupied by a surface exposed amino acid residue. The
 CC conjugate of the invention demonstrates antiatherosclerotic, antidiabetic,
 CC dermatological, immunosuppressive, immunomodulator and anorectic
 CC activities and may be useful for treating diabetes, obesity, atherosclerosis,
 CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC current sequence is that of the human adiponectin apm1 protein of the
 CC invention.
 XX SQ Sequence 144 AA:
 Query Match 100.0%; Score 708; DB 7; length 144;
 Best Local Similarity 100.0%; Pred. No. 4.1e-78;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FSVGLEYTVTIPNMPIRTKIFYNQHNYDGSTGKFCNPIGLYFAHYITVYMKDVKVS 60
 Db 15 FSVGLEYTVTIPNMPIRTKIFYNQHNYDGSTGKFCNPIGLYFAHYITVYMKDVKVS 74
 Qy 61 LFKKKDKAMLFYDQYQENNDQASGSVVLHLEVGDDQWLNQVYGEGERGLYADNDNSTF 120
 Db 75 LFKKKDKAMLFYDQYQENNDQASGSVVLHLEVGDDQWLNQVYGEGERGLYADNDNSTF 134

Db 178 TGFLYIYDTN 187

RESULT 10

XX ADE93614 standard; protein; 193 AA.

XX ID ADE93614;

XX AC

XX DT 12-FEB-2004 (first entry)

XX DE Human adiponectin apm1 (52-244) protein.

XX KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant; antirheumatic; antibacterial; antilipaemic; dermatological; immunosuppressive; immunomodulator; anorectic; diabetes; obesity; atherosclerosis; cardiovascular disease; dyslipidaemia; rheumatoic arthritis; Crohn's; systemic lupus erythematosus; sjogren syndrome; cachexia; septic shock; myasthenia gravis; myocardial infarction; inflammation; gene therapy; human; apm1; wild-type.

XX OS Homo sapiens.

XX PN WO2003055916-A2.

XX PD 10-JUL-2003.

XX PF 20-DEC-2002; 2002WO-DK000897.

XX PR 21-DEC-2001; 2001DK-00001952.

XX PR 21-DEC-2001; 2001US-0343482P.

XX PR 25-APR-2002; 2002DK-00000627.

XX PR 25-APR-2002; 2002US-0375492P.

XX PR 03-JUL-2002; 2002DK-00001036.

XX PR 03-JUL-2002; 2002US-0394117P.

XX PR 20-SEP-2002; 2002DK-00001395.

XX PR 20-SEP-2002; 2002US-0412169P.

XX PA (MAXY-) MAXYGEN APS.

XX PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T; Bognes A;

XX DR N-FSDB; ADE93616.

XX PT New conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety, useful for preparing a composition for treating a mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.

XX PS Claim 44; SEQ ID NO 12; 184pp; English.

XX The invention relates to a novel conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety covalently attached to the adiponectin polypeptide. The adiponectin polypeptide comprises an amino acid residue having an attachment group for the first non-polypeptide moiety which has been introduced in a position where the parent adiponectin is occupied by a surface exposed amino acid residue. The conjugate of the invention demonstrates antiarteriosclerotic, antidiabetic, cardiant, anti-inflammatory, antibacterial, antilipaemic, dermatological, immunosuppressive, immunomodulator and anorectic activities and may be useful for treating diabetes, obesity, atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoic arthritis, Crohn's disease, systemic lupus erythematosus, sjogren syndrome, cachexia, septic shock, myasthenia gravis, myocardial infarction and destructive processes related to activation of the inflammatory system, as well as during gene therapy procedures. The current sequence is that of the human adiponectin apm1 protein of the invention.

XX Sequence 193 AA;

XX PS

Query Match 100.0%; Score 708; DB 7; length 193;

Best Local Similarity 100.0%; Pred. No. 6. 1e-78; Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 FSVGLETVTTIPMPMPFTKIFKNQHQHYDGGTGFKNICPGLYFVHITYMKDVKVS 60

Db 64 FSVGLETVTTIPMPMPFTKIFKNQHQHYDGGTGFKNICPGLYFVHITYMKDVKVS 123

Db 61 LFKKDKAMLFDTQYQENNDQASGSTLHLLEVDQWLOVGEGERGLYIADNDSTF 120

Db 124 LFKDKAMLFDTQYQENNDQASGSTLHLLEVDQWLOVGEGERGLYIADNDSTF 183

Db 12-FEB-2004 (first entry)

Db 121 TGFLYIYDTN 130

Db 184 TGFLYIYDTN 193

RESULT 11

XX ID ADE93605 standard; protein; 203 AA.

XX AC ADE93605;

XX DT 12-FEB-2004 (first entry)

XX DE Human adiponectin apm1 (42-244) protein.

XX KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant; antirheumatic; antibacterial; antilipaemic; dermatological; immunosuppressive; immunomodulator; anorectic; diabetes; obesity; atherosclerosis; cardiovascular disease; dyslipidaemia; rheumatoic arthritis; Crohn's; systemic lupus erythematosus; sjogren syndrome; cachexia; septic shock; myasthenia gravis; myocardial infarction; inflammation; gene therapy; human; apm1; wild-type.

XX OS Homo sapiens.

XX PN WO2003055916-A2.

XX PD 10-JUL-2003.

XX PF 20-DEC-2002; 2002WO-DK000897.

XX PR 21-DEC-2001; 2001DK-00001952.

XX PR 21-DEC-2001; 2001US-0343482P.

XX PR 25-APR-2002; 2002DK-00000627.

XX PR 25-APR-2002; 2002US-0375492P.

XX PR 03-JUL-2002; 2002DK-00001036.

XX PR 03-JUL-2002; 2002US-0394117P.

XX PR 20-SEP-2002; 2002US-0412169P.

XX PA (MAXY-) MAXYGEN APS.

XX PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T; Bognes A;

XX DR

XX PT New conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety, useful for preparing a composition for treating a mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.

XX PS Claim 44; SEQ ID NO 3; 184pp; English.

XX The invention relates to a novel conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety covalently attached to the adiponectin polypeptide. The adiponectin polypeptide comprises an amino acid residue having an attachment group for the first non-polypeptide moiety which has been introduced in a position where the parent

CC adiponectin is occupied by a surface exposed amino acid residue. The
 CC conjugate of the invention demonstrates antiarteriosclerotic,
 CC anti-diabetic, cardiotropic, anti-rheumatic, anti-bacterial, anti-lipaemic,
 CC dermatological, immunosuppressive, immunomodulator and anorectic
 CC activities and may be useful for treating diabetes, obesity,
 CC arteriosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC current sequence is that of the human adiponectin apM1 protein of the
 CC invention.
 XX

SQ Sequence 203 AA;

Query Match 100.0%; Score 708; DB 7; Length 203;
 Best Local Similarity 100.0%; Pred. No. 6.5e-78; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSVGLETYVTPNMPIRFTKLYFQYQHNCYDSTGKFCNCNIDGLYFAVHITVVMKDVKVS 60
 DB 74 PSVGLETYVTPNMPIRFTKLYFQYQHNCYDSTGKFCNCNIDGLYFAVHITVVMKDVKVS 133

QY 61 LFKKDKAMLFYTDQYQENNNVQDQASGVLLHLEVGDQWLVQYGERNRGLYADNDNSTF 120
 DB 134 LFKKDKAMLFYTDQYQENNNVQDQASGVLLHLEVGDQWLVQYGERNRGLYADNDNSTF 193

QY 121 TGFLIYHDTN 130
 DB 194 TGFLIYHDTN 203

RESULT 12

ID ADE93604 standard; protein; 226 AA.

AC ADE93604;
 XX 12-FEB-2004 (first entry)

DB Human adiponectin apM1 (19-244) protein.

XX adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiotropic;
 KW anti-inflammatory; anti-microbial; anti-lipaemic; dermatological;
 KW atherosclerosis; cardiovascular diseases; dyslipidaemia; rheumatoid
 KW arthritis; Crohn's disease; systemic lupus erythematosus; Sjogren
 KW syndrome; cachexia; septic shock; myasthenia gravis; myocardial
 KW infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures.
 CC current sequence is that of the human adiponectin apM1 protein of the
 CC invention.
 XX

SQ Sequence 226 AA;

Query Match 100.0%; Score 708; DB 7; Length 226;
 Best Local Similarity 100.0%; Pred. No. 7.5e-78; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSVGLETYVTPNMPIRFTKLYFQYQHNCYDSTGKFCNCNIDGLYFAVHITVVMKDVKVS 60
 DB 97 PSVGLETYVTPNMPIRFTKLYFQYQHNCYDSTGKFCNCNIDGLYFAVHITVVMKDVKVS 156

QY 61 LFKKDKAMLFYTDQYQENNNVQDQASGVLLHLEVGDQWLVQYGERNRGLYADNDNSTF 120
 DB 157 LFKKDKAMLFYTDQYQENNNVQDQASGVLLHLEVGDQWLVQYGERNRGLYADNDNSTF 216

QY 121 TGFLIYHDTN 130
 DB 217 TGFLIYHDTN 226

RESULT 13

ID AAY21808 standard; protein; 231 AA.

XX AAY21808;
 AC AAY21808;
 XX
 DT 10-SEP-1999 (first entry)

XX DE Adipose most abundant gene transcription product 1 (apM1) fragment.

XX Smooth muscle proliferation; secretion factor; apM1; adipose;
 KW adipose most abundant gene transcription product 1; obesity;
 KW arteriosclerosis; restenosis; angina pectoris; myocardial infarction.
 KW Unidentified.

XX WO9921577-A1.

XX 06-MAY-1999.

XX PP 27-OCT-1998; 98W0-JP004862.

XX BR 29-OCT-1997; 97JP-00297569.

XX PA (SAKA) OTSUKA PHARM CO LTD.

XX Matsumawa Y, Ohmoto Y;

PI Rasmussen PB, Andersen KV, Pedersen AH, Schambrey HT, Halkier T;

XX
DR WPI; 1999-418412/35.

XX
PT Inhibition of smooth muscle proliferation using secretion factor apM1.

XX
PS Example; Page 59-60; 65pp; Japanese.

XX
CC Then invention relates to the inhibition of smooth muscle proliferation using a composition containing secretion factor apM1 (adipose most abundant gene transcript 1), together with a suitable carrier. apM1 is expressed specifically in adipose tissue and the composition is used for the prevention and treatment of arteriosclerosis; restenosis following vascular reconstruction; and treatment and diagnosis of diseases related to obesity, and disorders associated with it such as angina pectoris and myocardial infarction. The present sequence represents a fragment of apM1 isolated from abdominal fat tissue of myoma user.

XX
CC Sequence 231 AA;

Query Match 100.0%; Score 708; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 7.8e-78; Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETYVTPNPPIRFKIFPQNQHGSTOKPHCNIPGLYFAVHITVVKDKVKS 60
Db 102 FSVGLETYVTPNPPIRFKIFPQNQHGSTOKPHCNIPGLYFAVHITVVKDKVKS 161

QY 61 LFKKDKAMLFYDQYQENNDQASGSVILHLEVGQWNLQVYGERGNGLYADNDNSTF 120
Db 162 LFKKDKAMLFYDQYQENNDQASGSVILHLEVGQWNLQVYGERGNGLYADNDNSTF 221

QY 121 TGFLLYHDIN 130
Db 222 TGFLLYHDIN 231

RESULT 15

ADD93530 ID ADD93530 standard; protein; 233 AA.
XX AC ADD93530;
XX DT 29-JAN-2004 (first entry)

XX DE Novel NOV2e, homologous to human adiponectin.

XX KW NOV2e; human; adiponectin; gene therapy.

XX OS Homo sapiens.
XX PN WO2003078572-A2.

XX PD 25-SEP-2003.

XX PF 06-MAR-2003; 2003WO-US006659.

XX PR 15-MAR-2002; 2002US-0365034P.

XX PR 19-MAR-2002; 2002US-0365477P.

XX PR 21-MAR-2002; 2002US-0366410P.

XX PR 05-MAR-2003; 2003US-00379747.

XX PA (CURA-) CURAGEN CORP.

XX PI Burgess CE, Chant JS, Chaudhuri A, Edinger SR, Ganguli EA; PT Malyanur UM, Miller CE, Ooi CE, Ort T, Paturajan M, Rastelli L; PT Rieger DK, Shinkets RA, Zerhusen BD;

XX DR WPI; 2003-779122/73.

XX PR (SAKA) OTSUKA PHARM CO LTD.

XX DR WPI; 2001-127687/14.

XX PT Detection of an antigenic protein comprises use of enzyme linked immunosorbant assay.

XX PS Example 1; Page 7-8; 10pp; Japanese.

XX CC The invention relates to a method for detecting an antigenic protein. The

CC method comprises boiling the sample containing the antigenic protein in the presence of sodium sulphate, diluting it in buffer, and detecting the enzyme by enzyme-linked immunosorbant assay (ELISA). In an exemplification of the invention, residues 15-244 (plus an initial Met residue) of human apM1 (adipose most abundant gene transcript 1; ADD9347), an adipose-specific collagen-like factor, was recombinantly expressed in *Escherichia coli*. Using the method of the invention, it was found that apM1 was expressed mainly in the inclusion body fragment as an approximately 30 kd protein. The present sequence represents the recombinantly expressed human apM1.

XX Sequence 231 AA;

Query Match 100.0%; Score 708; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 7.8e-78; Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETYVTPNPPIRFKIFPQNQHGSTOKPHCNIPGLYFAVHITVVKDKVKS 60
Db 102 FSVGLETYVTPNPPIRFKIFPQNQHGSTOKPHCNIPGLYFAVHITVVKDKVKS 161

QY 61 LFKKDKAMLFYDQYQENNDQASGSVILHLEVGQWNLQVYGERGNGLYADNDNSTF 120
Db 162 LFKKDKAMLFYDQYQENNDQASGSVILHLEVGQWNLQVYGERGNGLYADNDNSTF 221

QY 121 TGFLLYHDIN 130
Db 222 TGFLLYHDIN 231

RESULT 14

ADD93530 ID ADD93530 standard; protein; 231 AA.
XX AC ADD93530;
XX DT 29-JAN-2004 (first entry)

XX DE Novel NOV2e, homologous to human adiponectin.

XX KW NOV2e; human; adiponectin; gene therapy.

XX OS Homo sapiens.

XX PN WO2003078572-A2.

XX PD 25-SEP-2003.

XX PF 06-MAR-2003; 2003WO-US006659.

XX PR 15-MAR-2002; 2002US-0365034P.

XX PR 19-MAR-2002; 2002US-0365477P.

XX PR 21-MAR-2002; 2002US-0366410P.

XX PR 05-MAR-2003; 2003US-00379747.

XX PA (CURA-) CURAGEN CORP.

XX PI Burgess CE, Chant JS, Chaudhuri A, Edinger SR, Ganguli EA;

PT Malyanur UM, Miller CE, Ooi CE, Ort T, Paturajan M, Rastelli L;

PT Rieger DK, Shinkets RA, Zerhusen BD;

XX DR WPI; 2003-779122/73.

XX PR (SAKA) OTSUKA PHARM CO LTD.

XX DR WPI; 2001-127687/14.

XX PT Detection of an antigenic protein comprises use of enzyme linked immunosorbant assay.

XX PS Example 1; Page 7-8; 10pp; Japanese.

XX CC The invention relates to a method for detecting an antigenic protein. The

CC adiponectin (adipose most abundant gene transcript 1, APM1). The CC adiponectin gene is the most abundant gene transcript in adipose cells CC that regulates lipid metabolism. An interaction between adiponectin and calcium modulating ligand was identified, indicating a novel pathway by CC which adiponectin may induce lipid breakdown in muscle cells and CC adipocytes. The invention is based on the identification of proteins and CC polypeptides, and the nucleic acids encoding them, that are CC differentially modulated in a pathological state, disease or an abnormal CC condition or state. These are targets for therapeutic agents and can be CC used in screening methodologies to identify candidate therapeutic agents CC which interact with the target and thereby exert a desired or favourable CC effect, e.g. in neurogenesis, cell differentiation, cell proliferation, CC haematopoiesis, wound healing and angiogenesis. Methods for diagnosis, CC treatment and prevention of disorders involving the novel human nucleic CC acids and proteins are provided. The polypeptides are also used to raise CC antibodies, useful in therapy and diagnosis.

XX Sequence 233 AA;

Query Match 100 %; Score 708; DB 7; Length 233;
 Best Local Similarity 100 %; Pred. No. 7.9e-78; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	PSVGLIERYVTIPNMPIRFTKIPYNGQHNPYDSTGKPHCNITPGLYFPAVHITVYMKDVKS	60
Db	104	PSVGLIERYVTIPNMPIRFTKIPYNGQHNPYDSTGKPHCNITPGLYFPAVHITVYMKDVKS	163
QY	61	LPKKDKAMLFYDQKQENNVQASGSVLLHEEVGDQWLQTYGEGERGLYIADNDNSTF	120
Db	164	LPKKDKAMLFYDQKQENNVQASGSVLLHEEVGDQWLQTYGEGERGLYIADNDNSTF	223
QY	121	TGFLLYHDIN	130
Db	224	TGFLLYHDIN	233

Search completed: May 6, 2005, 17:22:12
 Job time : 79.0651 secs

Copyright (c) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 8, 2005, 13:27:58 ; Search time 55.967 Seconds
(without alignment)
774.883 Million cell updates/sec

Title: US-10-072-159-11
Perfect score: 708
Sequence: FSVGLEYTVTINMPIRFTK. YADNDNDSTFGFLYHDTN 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1428581 seqs, 333598853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6_ptodata/1/pubpaa/us07_PUBCOMB.pep:*

2: /cgn2_6_ptodata/1/pubpaa/pct_NEW_PUB.pep:*

3: /cgn2_6_ptodata/1/pubpaa/us05_PUB.pep:*

4: /cgn2_6_ptodata/1/pubpaa/us06_PUBCOMB.pep:*

5: /cgn2_6_ptodata/1/pubpaa/us07_PUB.pep:*

6: /cgn2_6_ptodata/1/pubpaa_pctrus_PUBCOMB.pep:*

7: /cgn2_6_ptodata/1/pubpaa/us08_PUB.pep:*

8: /cgn2_6_ptodata/1/pubpaa/us08_PUBCOMB.pep:*

9: /cgn2_6_ptodata/1/pubpaa_us09_PUBCOMB.pep:*

10: /cgn2_6_ptodata/1/pubpaa_us09_PUBCOMB.pep:*

11: /cgn2_6_ptodata/1/pubpaa_us09c_PUBCOMB.pep:*

12: /cgn2_6_ptodata/1/pubpaa_us09_NEW_PUB.pep:*

13: /cgn2_6_ptodata/1/pubpaa/us10_PUBCOMB.pep:*

14: /cgn2_6_ptodata/1/pubpaa/us10c_PUBCOMB.pep:*

15: /cgn2_6_ptodata/1/pubpaa/us10c_PUBCOMB.pep:*

16: /cgn2_6_ptodata/1/pubpaa_us10_PUBCOMB.pep:*

17: /cgn2_6_ptodata/1/pubpaa_us10_NEW_PUB.pep:*

18: /cgn2_6_ptodata/1/pubpaa_us11_NEW_PUB.pep:*

19: /cgn2_6_ptodata/1/pubpaa_us60_NEW_PUB.pep:*

20: /cgn2_6_ptodata/1/pubpaa_us60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	708	100.0	130	13 US-10-072-159-11	Sequence 11, Appl
2	708	100.0	130	13 US-10-060-845-11	Sequence 11, Appl
3	708	100.0	130	13 US-10-325-71-7	Sequence 7, Appl
4	708	100.0	137	14 US-10-325-71-7	Sequence 7, Appl
5	708	100.0	144	14 US-10-325-71-7	Sequence 5, Appl
6	708	100.0	145	14 US-10-325-71-11	Sequence 11, Appl
7	708	100.0	157	14 US-10-325-71-4	Sequence 4, Appl
8	708	100.0	160	17 US-10-655-782-23	Sequence 23, Appl
9	708	100.0	163	14 US-10-325-71-10	Sequence 10, Appl
10	708	100.0	163	14 US-10-325-71-53	Sequence 53, Appl
11	708	100.0	187	14 US-10-325-71-13	Sequence 13, Appl
12	708	100.0	193	14 US-10-325-71-12	Sequence 12, Appl
13	708	100.0	203	14 US-10-325-71-3	Sequence 3, Appl

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 2
US-10-060-845-11

; Sequence 11, Application US/10060845
; Publication No. US20020165154A1
; GENERAL INFORMATION:
; APPLICANT: Bihain, Bernard
; APPLICANT: Bougnelert, Lydie
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: Lipoprotein-regulating medicaments
; CURRENT APPLICATION NUMBER: US/10/060,845
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: U.S. 09/485,316
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: FR 97/10088
; PRIOR FILING DATE: 1997-08-06
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: PCT IB98/01256
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent.pm
; SEQ ID NO 11
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: 1..130
; OTHER INFORMATION: fragment 115..244 of translation from ref Genbank D45371

Query Match 100.0%; Score 708; DB 13; Length 130;
Best Local Similarity 100.0%; Pred. No. 4.4e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLEYTIVTIPNMPIRFTKIFYNQONHYDOSTGKPHCNIPGLYFAVHITVYMKDVKS 60
1 FSVGLEYTIVTIPNMPIRFTKIFYNQONHYDOSTGKPHCNIPGLYFAVHITVYMKDVKS 60
Db 61 LFKKOKAMLFYDQVQENNVDQASGSVLUHLLEVGDQVWILQVYGERNGLYADNDNSTF 120
QY 61 LFKKOKAMLFYDQVQENNVDQASGSVLUHLLEVGDQVWILQVYGERNGLYADNDNSTF 120
Db 61 LFKKOKAMLFYDQVQENNVDQASGSVLUHLLEVGDQVWILQVYGERNGLYADNDNSTF 120
QY 121 TGFLLYHDTN 130
Db 121 TGFLLYHDTN 130

RESULT 3
US-10-325-717-7

; Sequence 7, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbø
; APPLICANT: Andersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bøgesøe, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 021518610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apm1(108-244)
; US-10-325-717-6

Query Match 100.0%; Score 708; DB 14; Length 137;
Best Local Similarity 100.0%; Pred. No. 4.7e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-10-325-717-6

; Sequence 6, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbø
; APPLICANT: Andersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bøgesøe, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 021518610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apm1(108-244)

Query Match 100.0%; Score 708; DB 14; Length 137;
Best Local Similarity 100.0%; Pred. No. 4.7e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
TITLE OF INVENTION: Adiponectin Fragments and Conjugates
FILE REFERENCE: 0251ue610

Query Match 100.0%; Score 708; DB 14; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5. 5e-70;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLEYTYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNCNIPGLYFAVHITVYMKDVKS 60
 28 FSVGLEYTYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNCNIPGLYFAVHITVYMKDVKS 87

Db 61 LFKKDKAMLFYDQYQENNNDQASGSVLLHLEVGQWLVQYGEGERNGLYADNDNSTP 120

QY 88 LFKKDKAMLFYDQYQENNNDQASGSVLLHLEVGQWLVQYGEGERNGLYADNDNSTP 147

Db 121 TGFLLYHDTN 130
 148 TGFLLYHDTN 157

RESULT 8
 US-10-659-782A-23
 ; Sequence 23, Application US/10659782A
 ; Publication No. US20050059015A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mintz, Liat
 ; TITLE OF INVENTION: Compositions, Reagents and Kits for and Methods of Diagnosing, Monitoring and Treating Obesity and/or Diabetes
 ; FILE REFERENCE: 2823B
 ; CURRENT APPLICATION NUMBER: US/10/659,782A
 ; CURRENT FILING DATE: 2003-09-11
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 23
 ; LENGTH: 160
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-659-782A-23

Query Match 100.0%; Score 708; DB 17; Length 160;
 Best Local Similarity 100.0%; Pred. No. 5. 7e-70;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLEYTYVTIPNMPTRFTKIFYNQONHYDGSTGKFCNCNIPGLYFAVHITVYMKDVKS 60
 31 FSVGLEYTYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNCNIPGLYFAVHITVYMKDVKS 90

Db 61 LFKKDKAMLFYDQYQENNNDQASGSVLLHLEVGQWLVQYGEGERNGLYADNDNSTP 120

QY 91 LFKKDKAMLFYDQYQENNNDQASGSVLLHLEVGQWLVQYGEGERNGLYADNDNSTP 150

Db 121 TGFLLYHDTN 130
 151 TGFLLYHDTN 160

RESULT 9
 US-10-325-717-10
 ; Sequence 10, Application US/10325717
 ; Publication No. US20030176328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rasmussen, Poul Baad
 ; APPLICANT: Andersen, Kim Vilbourn
 ; APPLICANT: Pedersen, Anders Hjelholt
 ; APPLICANT: Schambye, Hans Thalsgaard
 ; APPLICANT: Halkier, Torben
 ; APPLICANT: Bøghes, Are
 ; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
 ; FILE REFERENCE: 0251us610
 ; CURRENT APPLICATION NUMBER: US/10/325,717
 ; CURRENT FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: US 60/412,169
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: US 60/394,117
 ; PRIOR FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: US 60/375,492
 ; PRIOR FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: US 60/343,482
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 53
 ; LENGTH: 163
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic construct Y11N-apM1 (82-244)
 ; US-10-325-717-53

Query Match 100.0%; Score 708; DB 14; Length 163;
 Best Local Similarity 100.0%; Pred. No. 5. 8e-70;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLEYTYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNCNIPGLYFAVHITVYMKDVKS 60
 Db 34 FSVGLEYTYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNCNIPGLYFAVHITVYMKDVKS 93

QY 61 LFKKDKAMLFYDQYQENNNDQASGSVLLHLEVGQWLVQYGEGERNGLYADNDNSTP 120

Db 61 LFKKDKAMLFYDQYQENNNDQASGSVLLHLEVGQWLVQYGEGERNGLYADNDNSTP 153

Db 121 TGFLLYHDTN 130
 154 TGFLLYHDTN 163

RESULT 10
 US-10-325-717-53
 ; Sequence 53, Application US/10325717
 ; Publication No. US20030176328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rasmussen, Poul Baad
 ; APPLICANT: Andersen, Kim Vilbourn
 ; APPLICANT: Pedersen, Anders Hjelholt
 ; APPLICANT: Schambye, Hans Thalsgaard
 ; APPLICANT: Halkier, Torben
 ; APPLICANT: Bøghes, Are
 ; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
 ; FILE REFERENCE: 0251us610
 ; CURRENT APPLICATION NUMBER: US/10/325,717
 ; CURRENT FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: US 60/412,169
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: US 60/394,117
 ; PRIOR FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: US 60/375,492
 ; PRIOR FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: US 60/343,482
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 53
 ; LENGTH: 163
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic construct Y11N-apM1 (82-244)
 ; US-10-325-717-53

Query Match 100.0%; Score 708; DB 14; Length 163;
 Best Local Similarity 100.0%; Pred. No. 5. 8e-70;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLEYTYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNCNIPGLYFAVHITVYMKDVKS 60
 Db 34 FSVGLEYTYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNCNIPGLYFAVHITVYMKDVKS 93

QY 61 LFKKDKAMLFYDQYQENNNDQASGSVLLHLEVGQWLVQYGEGERNGLYADNDNSTP 120

RESULT 11
 US-10-325-717-13
 ; Sequence 13, Application US/10325717
 ; Publication No. US2003017632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rasmussen, Poul Baad
 ; APPLICANT: Andersen, Kim Vilbour
 ; APPLICANT: Pedersen, Anders Hjelholt
 ; APPLICANT: Schambye, Hans Thalsgaard
 ; APPLICANT: Halkier, Torben
 ; APPLICANT: Bognes, Are
 ; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
 ; FILE REFERENCE: 051us610
 ; CURRENT APPLICATION NUMBER: US/10/325,717
 ; CURRENT FILING DATE: 2002-12-20
 ; PRIORITY NUMBER: US 60/412,169
 ; PRIORITY FILING DATE: 2002-09-20
 ; PRIORITY APPLICATION NUMBER: US 60/394,117
 ; PRIORITY FILING DATE: 2002-07-03
 ; PRIORITY APPLICATION NUMBER: US 60/375,492
 ; PRIORITY FILING DATE: 2002-04-25
 ; PRIORITY APPLICATION NUMBER: US 60/343,482
 ; PRIORITY FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: apM1(52-244)

US-10-325-717-12
 Query Match 100.0%; Score 708; DB 14; Length 193;
 Best Local Similarity 100.0%; Pred. No. 7. 2e-10;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FSVGLETVTIPNMPIRFTKIFYNQHNYDGSTGKFCNCIPGLYFAVHITYMKDKVKS 60
 Db 64 FSVGLETVTIPNMPIRFTKIFYNQHNYDGSTGKFCNCIPGLYFAVHITYMKDKVKS 123
 Qy 61 LFKKDKKAMLFITYQOENNDQASGSVVLHLEVGQWMLQVYCEGERGLYADNDNSTF 120
 Db 124 LFKKDKKAMLFITYQOENNDQASGSVVLHLEVGQWMLQVYCEGERGLYADNDNSTF 183
 Qy 121 TGFLLYHDTN 130
 Db 184 TGFLLYHDTN 193

RESULT 12
 US-10-325-717-12
 ; Sequence 12, Application US/10325717
 ; Publication No. US2003017632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rasmussen, Poul Baad
 ; APPLICANT: Andersen, Kim Vilbour
 ; APPLICANT: Pedersen, Anders Hjelholt
 ; APPLICANT: Schambye, Hans Thalsgaard
 ; APPLICANT: Halkier, Torben
 ; APPLICANT: Bognes, Are
 ; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
 ; FILE REFERENCE: 051us610
 ; CURRENT APPLICATION NUMBER: US/10/325,717
 ; CURRENT FILING DATE: 2002-12-20
 ; PRIORITY NUMBER: US 60/412,169
 ; PRIORITY FILING DATE: 2002-09-20
 ; PRIORITY APPLICATION NUMBER: US 60/394,117
 ; PRIORITY FILING DATE: 2002-07-03
 ; PRIORITY APPLICATION NUMBER: US 60/375,492
 ; PRIORITY FILING DATE: 2002-04-25
 ; PRIORITY APPLICATION NUMBER: US 60/343,482
 ; PRIORITY FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 203
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: apM1(42-244)

US-10-325-717-3
 Query Match 100.0%; Score 708; DB 14; Length 203;
 Best Local Similarity 100.0%; Pred. No. 7. 6e-70;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FSVGLETVTIPNMPIRFTKIFYNQHNYDGSTGKFCNCIPGLYFAVHITYMKDKVKS 60

RESULT 14
 US-10-325-717-2
 ; Sequence 2, Application US/10325717
 ; Publication No. US20030176328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Basmussen, Poul Baad
 ; APPLICANT: Andersen, Kim Vilborg
 ; APPLICANT: Pedersen, Anders Hielholt
 ; APPLICANT: Schambye, Hans Thalsgaard
 ; APPLICANT: Halkier, Torben
 ; APPLICANT: Bognsnes, Are
 ; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
 ; FILE REFERENCE: 0251us610
 ; CURRENT APPLICATION NUMBER: US/10/325,717
 ; CURRENT FILING DATE: 2002-12-20
 ; PRIORITY APPLICATION NUMBER: US 60/412,169
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: US 60/394,117
 ; PRIOR FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: US 60/375,492
 ; PRIOR FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: US 60/343,482
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 226
 ; TYPE: PRT
 ; FEATURE:
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: apm1(19-244)
 ; US-10-325-717-2

Query Match 100.0%; Score 708; DB 14; Length 231;
 Best Local Similarity 100.0%; Pred. No. 8.7e-70; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 LFKKOKAMLFYDQOBNNVDOASGSVLLHLEVGDQWLVQYGEGERGLYADNDNSTF 120
 Db 134 LFKKOKAMLFYDQOBNNVDOASGSVLLHLEVGDQWLVQYGEGERGLYADNDNSTF 193
 QY 121 TGFLLYHDTN 130
 Db 194 TGFLLYHDTN 203

RESULT 15
 US-10-189-493-2
 ; Sequence 2, Application US/10189493
 ; Publication No. US2003016651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Otsuka Pharmaceutical Co., Ltd
 ; TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a
 ; TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit
 ; TITLE OF INVENTION: therefore
 ; FILE REFERENCE: P98-51
 ; CURRENT APPLICATION NUMBER: US/10/189,493

Query Match 100.0%; Score 708; DB 14; Length 231;
 Best Local Similarity 100.0%; Pred. No. 9e-70; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 LFKKOKAMLFYDQOBNNVDOASGSVLLHLEVGDQWLVQYGEGERGLYADNDNSTF 120
 Db 102 FSVGLETYVTPNMPIRFTKIFYNQHNGDSTGKPHCNIPGLYFAVHITVYMKDVKS 60
 QY 121 TGFLLYHDTN 130
 Db 162 LFKKOKAMLFYDQOBNNVDOASGSVLLHLEVGDQWLVQYGEGERGLYADNDNSTF 221
 QY 222 TGFLLYHDTN 231

Search completed: May 8, 2005, 15:47:33
 Job time : 56.967 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2005, 17:08:11 ; Search time 14.1497 Seconds
(without alignments)
883.992 Million cell updates/sec

Title: US-10-072-159-11
Perfect score: 708
Sequence: 1 FSVGLETVTIPNMPIRFTK. YADNDNDSTFGFLLYHDTN 130
Scoring table: BLOSUM2
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR 79;*

1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

RESULT 1
JC4708
gelatin-binding 28K protein precursor - human
N;Alternate name: adipose specific collagen-like factor
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: JC4708; JC4944
R;Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Matsuzawa, Y.; Matsubara, K.
Biochem. Biophys. Res. Commun. 221, 286-289, 1996
A;Title: cDNA cloning and expression of a novel adipose specific collagen-like factor,
A;Reference: PMID:96224171; PMID:8619847
A;Accession: JC4708
A;Molecule type: mRNA
A;Residues: 1-244 <MAE>
A;Cross-references: UNIPROT:Q15948; DDBJ:D45371; NID:9871886; PIDN:BA08227.1; PID:9871
A;Experimental source: adipose tissue
R;Nakano, Y.; Tobe, T.; Choi-Miura, N.H.; Mazda, T.; Tomita, M.
J. Biochem. 120, 803-812, 1996

ALIGNMENTS

Query Match 100.0% ; Score 708; DB 2; Length 244;
Best Local Similarity 100.0% ; Pred. No. 1 2e-63; Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVTIPNMPIRFTKIFVNQHQHYDGSTGKFCHEKNICPGLYFAVHTIVMKDKVVS 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
182.5 253 1 C1H0Q 115 FSVGLETVTIPNMPIRFTKIFVNQHQHYDGSTGKFCHEKNICPGLYFAVHTIVMKDKVVS 174
198 251 2 B48150 61 LFKDKAMLFYDQYQYENNDQASGSLHLEVGQWLOVGEGERGLYADNDNSTP 120
20 176 24.9 2 A48150 211 253 2 C48150 221 174 24.6 215 2 C48150 22 156 245 2 S19018 221 156 245 2 S19018 175 LFKDKAMLFYDQYQYENNDQASGSLHLEVGQWLOVGEGERGLYADNDNSTP 234
23 184 26.0 253 2 I49560 18 184 26.0 253 2 I49560 182.5 25.8 253 1 C1H0Q 115 FSVGLETVTIPNMPIRFTKIFVNQHQHYDGSTGKFCHEKNICPGLYFAVHTIVMKDKVVS 174
19 178 25.1 215 2 B48150 61 LFKDKAMLFYDQYQYENNDQASGSLHLEVGQWLOVGEGERGLYADNDNSTP 120
20 176 24.9 196 2 A48150 21 174 24.6 215 2 C48150 22 156 245 2 S19018 221 156 245 2 S19018 175 LFKDKAMLFYDQYQYENNDQASGSLHLEVGQWLOVGEGERGLYADNDNSTP 234
24 19.5 16.9 224 2 A46032 25 16.5 16.9 193 2 A37873 26 16.0 1228 2 A57384 27 13.5 12.2 213 2 B8J360 28 8.2 11.6 280 1 G70126 29 10.9 687 2 E69733
121 TGFLLYHDTN 130 ||||| ||||| |||||
Db 235 TGFLLYHDTN 244

RESULT 2

fibrinogen beta chain
alpha-mannosidase
hypothetical protein
hypothetical protein
lymphoid-specific
hypothetical protein
alpha-mannosidase
IgA-specific metal
phage-related protein
transcription factor
monophenol monooxy
cell surface glyco
ubiquitin-protein
ubiquitin-protein
hypothetical protein
hypothetical protein

S2297
 collagen alpha 1(X) chain precursor - chicken
 N;Alternate names: type X collagen
 C;Species: Gallus gallus (chicken)
 C;Date: 07-Oct-1994 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S2297; A31896; S65594; S7711; I50218
 R;Ninomiya, Y.; Castagnola, P.; Gercke, D.; Gordon, M.K.; Jacenko, O.; LuWalle, P.; MCC
 maguchi, N.; Olsen, B.R.
 in: Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pre
 A;Title: The molecular biology of collagens with short triple-helical domains.
 A;Reference number: S22243
 A;Accession: S22243
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-674 <NNI>
 A;Cross-references: UNIPROT:P08125
 R;LuWalle, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R.
 A;Title: The type X collagen gene. Intron sequences split the 5'-untranslated region and
 A;Reference number: A31896; MUID:89054019; PMID:2461368
 A;Accession: A31896
 A;Molecule type: mRNA
 A;Residues: 1-75 <LUT>
 R;Ninomiya, Y.; Gordon, M.; van der Rest, M.; Schmid, T.; Linsenmayer, T.; Olsen, B.R.
 A;Cross-references: EMBL:MI13496; NID:9211699; PIDN:AAA48736.1; PID:9211700
 A;Accession: S7711
 A;Molecule type: protein
 A;Residues: 104-112, X, 114-117, 453-466 <NNI>
 C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
 C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyproline;
 F;11-18/Domain: signal sequence #status predicted <SIG>
 F;547-673/Domain: complement C1q carboxyl-terminal homology <C1Q>
 F;533,455/Domain: modified site: hydroxyproline (Pro) #status experimental
 F;611/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 42.0%; Score 297.5; DB 2; Length 674;
 Best Local Similarity 47.6%; Pred. 6.8e-22;
 Matches 59; Conservative 21; Mismatches 43; Indels 1; Gaps 1;

QY 1 PSVGLETVTPNMPIRPTKFINQNHYDSTGKPHCNIPGLYPAVHITVVKDVKVS 60
 Db 548 PTVILSKAYPSATVPIKEDKLYNRCOHYDRTGIFTCRIPGLYVFSYHMTAKGTVWVA 607
 QY 61 IPKDKRMLFTYDQYQBNVVAQSGSVLHLFLEVGDQWLOVYGEGRNGLXADNDNSTF 120
 Db 608 LYKNGSPVWYTYDEYOKGYLQDQASGSAVIDMENDQWLOI-PNSBSNGLYSEVHSSF 666
 Qy 121 TGFL 124
 Db 667 SGFL 670

RESULT 3
 CGHUND
 collagen alpha 1(X) chain precursor - human
 N;Alternate names: procollagen alpha 1(X) chain
 C;Species: Homo sapiens (man)
 C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S23396; S30086; S15825; S18249; A43901; I51870; S21856
 R;Reichenberger, E.; Beier, F.; LuWalle, P.; Olsen, B.R.; von der Mark, K.; Bertling, W.
 A;Title: Genomic organization and full-length cDNA sequence of human collagen X.
 A;Reference number: S26396; MUID:93012005; PMID:139733
 A;Accession: S26396
 A;Molecule type: DNA
 A;Residues: 1-680 <REI>

A;Cross-references: UNIPROT:Q03692; EMBL:X69952; EMBL:X72578; EMBL:X72579; EMBL:X72580;
 R;Apte, S.S.
 A;Cross-references: EMBL:X65120; NID:931129
 A;Reference number: S30085
 A;Accession: S30085
 A;Molecule type: DNA
 A;Residues: 'TIPFGWGMVCLL', 52-680 <APT>
 A;Cross-references: EMBL:X65120; NID:931129
 A;Note: the initial difference is probably due to translation of an intronic sequence
 R;Apte, S.; Mattei, M.G.; Olsen, B.R.
 FEBS Lett. 282, 393-396, 1991
 A;Title: Cloning of human alpha-1(X) collagen DNA and localization of the COL10A1 gene t.
 A;Reference number: S15026; MUID:91243838; PMID:2037056
 A;Accession: S15026
 A;Molecule type: DNA
 A;Residues: 561-647, 'G', 649-666 <AP2>
 A;Cross-references: EMBL:X58979; NID:930013; PIDN:CAA41686.1; PID:930014
 R;Thomas, J.T.; Crosswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E.; Grant, M.
 Biochem. J. 280, 617-623, 1991
 A;Title: The human collagen X gene. Complete primary translated sequence and chromosomal
 A;Reference number: S18249; MUID:92109659; PMID:1764025
 A;Accession: S18249
 A;Molecule type: DNA
 A;Residues: 1-26, 'T', 28-680 <THO>
 A;Cross-references: EMBL:X63082; NID:930094; PIDN:CAA42933.1; PID:930095
 A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 532-Ala
 R;Wallis, G.A.; Rash, B.; Sweetman, W.A.; Thomas, J.T.; Super, M.; Evans, G.; Grant, M.B.
 Am. J. Hum. Genet. 54, 169-178, 1994
 R;Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, W.
 Dev. Biol. 148, 562-572, 1991
 A;Title: In situ hybridization studies on the expression of type X collagen in fetal hum
 A;Reference number: A43901; MUID:92077285; PMID:743401
 A;Accession: A43901
 A;Molecule type: mRNA
 A;Residues: 547-656 <RE2>
 A;Cross-references: GB:M74050; GB:D57494; NID:9339884; PIDN:AA61221.1; PID:9553796
 A;Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBI:69014)
 R;Wallis, G.A.; Rash, B.; Sweetman, W.A.; Thomas, J.T.; Super, M.; Evans, G.; Grant, M.B.
 Am. J. Hum. Genet. 54, 169-178, 1994
 A;Title: Amino acid substitutions of conserved residues in the carboxyl-terminal domain
 R;Schmid, P.; Mark, K.; Stoss, H.; Bertling, W.
 A;Reference number: 151870; MUID:94136476; PMID:8304336
 A;Accession: 151870
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 520-597, 'D', 599-680 <WAL>
 A;Cross-references: GB:68531; NID:9545180; PIDN:AC60615.1; PID:9545181
 A;Note: mutant sequence from patient with metaphyseal chondroplasia type Schmid
 C;Comment: a second mutant sequence with 614-Pro is also described
 C;Note: a second mutant sequence with 614-Pro is also described
 C;Comment: Prolines and Lysines at the third position of the tripeptide repeating unit (ed and subsequently O-glycosylated.
 C;Genetics:
 A;Gene: GDB:COL1A1
 A;Cross-references: GDB:128635; OMIM:120110
 A;Map position: 6q21-6q22
 A;Introns: 52/1
 A;Note: a defect in this gene may cause Schmid metaphyseal chondroplasia
 C;Complex: type X collagen may be a homotrimer
 C;Function:
 A;Description: structural component of extracellular fibrous polymer specifically and tr
 be important for skeletogenesis
 C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
 C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxylysine;
 R;1-18/Domain: signal sequence #status predicted <SIG>
 R;19-680/Domain: collagen alpha 1(X) chain #status predicted <MAT>
 R;19-56/Domain: amino-terminal nonhelical #status predicted <NC2>
 R;57-519/Domain: interrupted helical
 R;550-680/Domain: amino-terminal nonhelical #status predicted <NC1>
 R;553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>
 R;617/Domain: carbohydrate (Asn) (covalent) #status predicted
 Query Match 40.6%; Score 287.5; DB 1; Length 680;
 Best Local Similarity 46.4%; Pred. No. 6.9e-21;
 Matches 58; Conservative 19; Mismatches 47; Indels 1; Gaps 1;

A;Molecule type: DNA
 A;Residues: 1-743 <MUR>
 A;Cross-references: UNIPROT:Q00780; EMBL:X66976; NID:950493; PIDN:CAA47387.1; PID:913599
 C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology <CIQ>
 F;616-742/Domain: complement C1q carboxyl-terminal homology <CIQ>
 Query Match 38.6%; Score 273.5; DB 1; Length 743;
 Best Local Similarity 45.1%; Pred. No. 2e-19;
 Matches 55; Conservative 27; Mismatches 35; Indels 5; Gaps 2;
 QY 9 VTIPI---NMPIRFTKIFYQNYQHNGSTGKFCNCNTPGLYFAYHITVVMKDVKVLSLFKK 64
 Db 621 ITVPPPPVGAPVFKFDKLYNQYIYQNYQHNGSTGKFCNCNTPGLYFAYHITVVMKDVKVLSLFKK 64
 QY 65 DKAMLYPTYDQYQENNYDQASGSVLLTLEVGQWQVLYQVYIGERNGLYADNDNDSTPFGEL 124
 Db 681 NEPMWMTYDYEKKGFQDQASGSVAVLLRPGDQVFLQNPFB-QAAGLYAQYVHSSFSGYL 739
 QY 125 LY 126
 Db 740 LY 741

RESULT 7
 S15335
 collagen alpha 1(VIII) chain precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S15435
 R;Muragaki, Y.; Mattei, M.G.; Yamaguchi, N.; Olsen, B.R.; Ninomiya, Y.
 Bur. J. Biochem. 197, 65-622, 1991
 A;Title: The complete primary structure of the human alpha-1(VIII) chain and assignment
 A;Reference number: S15435; MUID:91231001; PMID:2029894
 A;Accession: S15435
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-744 <MUR>
 A;Cross-references: UNIPROT:P27658; EMBL:X57527; NID:930081; PIDN:CAA40748.1; PID:930082
 C;Genetics:
 A;Gene: GDB:COIA81
 A;Cross-references: GDB:128104; OMIM:120251
 A;Map position: 3q11.1-3q13.2
 C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology <CIQ>
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
 F;21-117/Region: amino-terminal nonhelical
 F;18-571/Region: interrupted helical
 F;572-743/Region: carboxyl-terminal nonhelical
 F;617-743/Domain: complement C1q carboxyl-terminal homology <CIQ>
 Query Match 37.2%; Score 270.5; DB 1; Length 744;
 Best Local Similarity 45.5%; Pred. No. 3.9e-19;
 Matches 51; Conservative 28; Mismatches 32; Indels 1; Gaps 1;
 QY 15 PIRFTKIFYQNYQHNGSTGKFCNCNTPGLYFAYHITVVMKDVKVLSLFKKMFTYDQ 74
 Db 632 PFKFDLRLYQDQASGSVAVLLRPGDQVFLQNPFB-QAAGLYAQYVHSSFSGYL 691
 QY 75 YQENNNDQASGSVLLTLEVGQWQVLYQVYIGERNGLYADNDNDSTPFGELLY 126
 Db 692 YKKGFLDQASGSVAVLLRPGDQVFLQNPFB-QAAGLYAQYVHSSFSGYL 742

RESULT 9
 S23298
 collagen alpha 1(VIII) chain - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: S23298
 R;Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; McC
 maguchi, N.; Olsen, B.R.
 in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp 79-114, Academic Pre
 A;Title: The molecular biology of collagens with short triple-helical domains.
 A;Reference number: S23298
 A;Accession: S23298
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-744 <NIN>
 A;Cross-references: UNIPROT:Q7LZR2
 C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology <CIQ>
 F;617-743/Domain: complement C1q carboxyl-terminal homology <CIQ>
 Query Match 37.2%; Score 263.5; DB 1; Length 744;
 Best Local Similarity 45.5%; Pred. No. 2e-18;
 Matches 51; Conservative 27; Mismatches 33; Indels 1; Gaps 1;
 QY 15 PIRFTKIFYQNYQHNGSTGKFCNCNTPGLYFAYHITVVMKDVKVLSLFKKMFTYDQ 74
 Db 632 PFKFDLRLYQDQASGSVAVLLRPGDQVFLQNPFB-QAAGLYAQYVHSSFSGYL 691
 QY 75 YQENNNDQASGSVLLTLEVGQWQVLYQVYIGERNGLYADNDNDSTPFGELLY 126
 Db 692 YKKGFLDQASGSVAVLLRPGDQVFLQNPFB-QAAGLYAQYVHSSFSGYL 742

RESULT 10
 B57131
 collagen alpha 2(VIII) chain - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C;Accession: B57131
 R;Muragaki, Y.; Jacenko, O.; Apté, S.; Mattei, M.G.; Ninomiya, Y.; Olsen, B.R.
 J. Biol. Chem. 266, 7721-7727, 1991
 A;Title: The alpha2(VIII) collagen gene. A novel member of the short chain collagen fami
 A;Reference number: B57131; MUID:9120292; PMID:2019595
 A;Accession: B57131
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-170 <MUR>
 A;Cross-references: UNIPROT:P25318; GB:M60833

RESULTS 8
 A34246
 collagen alpha 1(VIII) chain precursor - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: A34246
 R;Yamaguchi, N.; Banya, P.D.; van der Rest, M.; Ninomiya, Y.
 J. Biol. Chem. 264, 16022-16029, 1989
 A;Title: The cloning and sequencing of alpha1(VIII) collagen cDNAs demonstrate that type
 domains similar to those of type X collagen.

C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology

R;43-169/Domain: complement Clq carboxyl-terminal homology <Clq>

Query Match 36.5%; Score 258.5; DB 2; Length 170;

Best Local Similarity 40.8%; Pred. No. 1.1e-18; Matches 51; Conservative 27; Mismatches 46; Indels 1; Gaps 1;

A;Molecule type: mRNA

A;Residues: 1-219 <OTT>

A;Cross-references: UNIPROT:Q9BXJ0; EMBL:Al110261

A;Experimental source: adult uterus; Clone DKR2p58B0621

A;Genetics: A;Note: DKR2p58B0621.1

Query Match 34.4%; Score 243.5; DB 2; Length 219;

Best Local Similarity 42.1%; Pred. No. 4.7e-17; Matches 53; Conservative 23; Mismatches 45; Indels 5; Gaps 4;

A;Molecule type: mRNA

A;Residues: 1-219 <OTT>

A;Cross-references: UNIPROT:Q9BXJ0; EMBL:Al110261

A;Experimental source: adult uterus; Clone DKR2p58B0621

A;Genetics: A;Note: DKR2p58B0621.1

Query Match 34.4%; Score 243.5; DB 2; Length 219;

Best Local Similarity 42.1%; Pred. No. 4.7e-17; Matches 53; Conservative 23; Mismatches 45; Indels 5; Gaps 4;

A;Molecule type: mRNA

A;Residues: 1-219 <OTT>

A;Cross-references: UNIPROT:Q9BXJ0; EMBL:Al110261

A;Experimental source: adult uterus; Clone DKR2p58B0621

A;Genetics: A;Note: DKR2p58B0621.1

Query Match 34.4%; Score 243.5; DB 2; Length 219;

Best Local Similarity 42.1%; Pred. No. 4.7e-17; Matches 53; Conservative 23; Mismatches 45; Indels 5; Gaps 4;

A;Molecule type: mRNA

A;Residues: 1-219 <OTT>

A;Cross-references: UNIPROT:Q9BXJ0; EMBL:Al110261

A;Experimental source: adult uterus; Clone DKR2p58B0621

A;Genetics: A;Note: DKR2p58B0621.1

Query Match 34.4%; Score 243.5; DB 2; Length 219;

Best Local Similarity 42.1%; Pred. No. 4.7e-17; Matches 53; Conservative 23; Mismatches 45; Indels 5; Gaps 4;

A;Molecule type: mRNA

A;Residues: 1-219 <OTT>

A;Cross-references: UNIPROT:Q9BXJ0; EMBL:Al110261

A;Experimental source: adult uterus; Clone DKR2p58B0621

A;Genetics: A;Note: DKR2p58B0621.1

Query Match 34.4%; Score 243.5; DB 2; Length 219;

Best Local Similarity 42.1%; Pred. No. 4.7e-17; Matches 53; Conservative 23; Mismatches 45; Indels 5; Gaps 4;

A;Molecule type: mRNA

A;Residues: 1-219 <OTT>

A;Cross-references: UNIPROT:Q9BXJ0; EMBL:Al110261

A;Experimental source: adult uterus; Clone DKR2p58B0621

A;Genetics: A;Note: DKR2p58B0621.1

Query Match 34.4%; Score 243.5; DB 2; Length 219;

Best Local Similarity 42.1%; Pred. No. 4.7e-17; Matches 53; Conservative 23; Mismatches 45; Indels 5; Gaps 4;

A;Molecule type: mRNA

A;Residues: 1-219 <OTT>

A;Cross-references: UNIPROT:Q9BXJ0; EMBL:Al110261

A;Experimental source: adult uterus; Clone DKR2p58B0621

A;Genetics: A;Note: DKR2p58B0621.1

Query Match 34.4%; Score 243.5; DB 2; Length 219;

Best Local Similarity 42.1%; Pred. No. 4.7e-17; Matches 53; Conservative 23; Mismatches 45; Indels 5; Gaps 4;

A;Molecule type: mRNA

A;Residues: 1-219 <OTT>

A;Cross-references: UNIPROT:Q9BXJ0; EMBL:Al110261

A;Experimental source: adult uterus; Clone DKR2p58B0621

A;Genetics: A;Note: DKR2p58B0621.1

Query Match 34.4%; Score 243.5; DB 2; Length 219;

Best Local Similarity 40.8%; Pred. No. 1.6e-14; Matches 53; Conservative 22; Mismatches 47; Indels 8; Gaps 5;

A;Molecule type: mRNA

A;Residues: 1-219 <OTT>

A;Cross-references: UNIPROT:Q9BXJ0; EMBL:Al110261

A;Experimental source: adult uterus; Clone DKR2p58B0621

A;Genetics: A;Note: DKR2p58B0621.1

Query Match 34.4%; Score 243.5; DB 2; Length 219;

Best Local Similarity 42.1%; Pred. No. 4.7e-17; Matches 53; Conservative 23; Mismatches 45; Indels 5; Gaps 4;

A;Molecule type: mRNA

A;Residues: 1-219 <OTT>

A;Cross-references: UNIPROT:Q9BXJ0; EMBL:Al110261

A;Experimental source: adult uterus; Clone DKR2p58B0621

A;Genetics: A;Note: DKR2p58B0621.1

Query Match 34.4%; Score 243.5; DB 2; Length 219;

Best Local Similarity 42.1%; Pred. No. 4.7e-17; Matches 53; Conservative 23; Mismatches 45; Indels 5; Gaps 4;

A;Molecule type: mRNA

A;Residues: 1-219 <OTT>

A;Cross-references: UNIPROT:Q9BXJ0; EMBL:Al110261

A;Experimental source: adult uterus; Clone DKR2p58B0621

A;Genetics: A;Note: DKR2p58B0621.1

Search completed: May 6, 2005, 17:30:49
Job time : 16.1497 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: May 6, 2005, 17:05:46 ; Search time 49.9028 Seconds
(without alignments)
1333.999 Million cell updates/sec

Title: US-10-072-159-11

Perfect score: 708
Sequence: 1 FSVGLETYVTPNMPIRFTK..... YADNDNDSTPTGFLYHDTN 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	708	100.0	244 1 APM1_HUMAN	Q15848 homo sapien
2	707	99.9	2 0950577	Q55Jd7 macaca mulu
3	661	93.4	2 Q8K3R4	Q8K3R4 rattus norv
4	655	92.5	247 1 APM1_MOUSE	Q60994 mus musculus
5	655	92.5	247 2 Q8BHW2	Q8BHW2 mus musculus
6	633	89.4	244 1 Q76C76	Q76C76 canis familiaris
7	615	86.9	240 2 Q95H04	Q95H04 bos taurus
8	594	83.9	242 2 Q6Q2K6	Q6Q2K6 sus scrofa
9	594	83.9	243 2 Q6PP07	Q6PP07 sus scrofa
10	586	82.8	243 2 Q7YKF8	Q7YKF8 sus scrofa
11	557	78.7	244 2 Q6QW87	Q6QW87 gallus gallus
12	514	72.6	194 2 Q95H95	Q95H95 canis familiaris
13	501	70.8	235 2 Q6D145	Q6D145 xenopus laevis
14	478	67.5	235 2 Q6GJS9	Q6GJS9 xenopus laevis
15	464	65.5	153 2 Q6JRS5	Q6JRS5 sus scrofa
16	415	58.6	144 2 Q6V9B4	Q6V9B4 sus scrofa
17	363	51.3	106 2 Q6Z226	Q6Z226 felis silvestris
18	355	50.2	333 2 Q8ITW4	Q8ITW4 homo sapiens
19	345	48.8	195 2 Q8BZS3	Q8BZS3 mus musculus
20	310	43.8	145 2 Q6VF79	Q6VF79 bus scrofa
21	297	42.0	674 1 QAL_A_CHICK	QAL_A_CHICK
22	287	40.6	680 1 CA1A_HUMAN	CA1A_HUMAN
23	286	40.4	419 1 COLE_LEPMA	COLE_LEPMA
24	285	39.9	675 2 Q9N178	Q9N178 leponotus maculatus
25	281	39.8	295 2 Q9Z1K4	Q9Z1K4 rattus norvegicus
26	281	39.7	508 1 QTO1_ONCKE	QTO1_ONCKE
27	280	39.6	674 1 CALA_BOVIN	CALA_BOVIN
28	280	39.6	680 1 CALA_MOUSE	CALA_MOUSE
29	280	39.6	743 1 CALA_MOUSE	CALA_MOUSE
30	280	39.6	744 2 Q921S8	Q921S8 mus musculus
31	280	39.6	Q8BGL6	Q8BGL6 mus musculus

ALIGNMENTS

RESULT 1	APM1_HUMAN	STANDARD;	PRT;	244 AA.
ID	Q15848;			
AC				
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	25-JAN-2005 (Rel. 46, Last annotation update)			
DE	adiponectin precursor (Adipocyte, Ctg and collagen domain containing protein) (30 kDa adipocyte complement-related protein) (ACRP30)			
DE	(Adipose most abundant gene transcript 1) (apm-1) (Gelatin-binding protein)			
DE	Name=ACRP30, APM1, GBP28;			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC				
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-Adipose tissue;			
RA	MEDLINE=96224171; PubMed=8619847; DOI=10.1006/bbrc.1996.0587;			
RA	Maeda K., Okubo K., Shimomura T., Funahashi T., Matsuzawa Y., Matsubara K.;			
RA	Matsubara K.;			
RT	CDNA cloning and expression of a novel adipose specific collagen-like factor, apm1 (Adipose Most abundant Gene transcript 1);			
RT	factor, apm1 (Adipose Most abundant Gene transcript 1);			
RL	Biochem. Biophys. Res. Commun. 221:286-289(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=99196984; PubMed=10095105; DOI=10.1016/S0378-1119(99)00041-4;			
RA	Saito K., Tobe T., Minoshima S., Asakawa S., Sumiya J., Yoda M., Nakano Y., Shimizu N., Tomita M.;			
RA	Nakano Y., Shimizu N., Tomita M.;			
RL	Gene 229:67-73(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=99336939; PubMed=10403784; DOI=10.1006/bbrc.1999.0865;			
RA	Schaeffler A., Orbo E., Paitzsch K.D., Buechner C., Dronik W., Fuerst A., Schoellmerich J., Schmitz G.;			
RA	"The human apm-1, an adipocyte-specific gene linked to the family of TNF- β and to genes expressed in activated T cells, is mapped to chromosome 1q21.3-q23, a susceptibility locus identified for familial combined hyperlipidemia (FCH)";			
RT	chromosome 1q21.3-q23, a susceptibility locus identified for familial combined hyperlipidemia (FCH);			
RT	Biophys. Res. Commun. 260:416-425(1999).			
RL	[4]			
RP	SEQUENCE OF 19-33.			
RA	PubMed=15340161; DOI=10.1110/ps.04682504;			
RA	Zhang Z., Henzel W.J.;			
RT	"Signal peptide prediction based on analysis of experimentally verified cleavage sites." J. Protein Sci. 13:2819-2824(2004).			
RL	[5]			
RP	SEQUENCE OF N-TERMINUS, AND PARTIAL SEQUENCE.			
RA	PubMed=8941845;			
RA	Nakano Y., Tobe T., Choi-Miura N.H., Mada T., Tomita M.;			
RT	"Isolation and characterization of GBP28, a novel gelatin-binding			

RT protein purified from human plasma.";

RL J. Biochem. 120:803-812(1996).

RN [16] CHARACTERIZATION.

RX MEDLINE=2417747; PubMed=10963870;

RA Ouchi N., Kihara S., Funahashi T., Tenner A.J., Tomiyama Y., Matsuyama A., Matsuzawa Y.;

RA Matsuyama T., Oritani K., Takahashi T., Ishikawa J., Tomiyama Y.,

RA "Adiponectin, a new member of the family of soluble defense collagens, negatively regulates the growth of myelomonocytic progenitors and the functions of macrophages.";

RT Blood 96:1723-1732(2000).

RN [7] FUNCTION.

RX MEDLINE=21372498; PubMed=11479627; DOI=10.1038/90984;

RA Yamauchi T., Kamon J., Waki H., Terauchi Y., Kubota N., Hara K., Mori Y., Ide T., Murakami K., Tsuboyama-Kasakawa N., Ezaki O., Akamatsu Y., Gavrilova O., Vinson C., Reitman M.L., Kaechika H., Nakamatsu T., Yamashita S., Funahashi T., Matsuzawa Y.;

RA Hotta K., Nishida M., Takahashi M., Muraguchi M., Ohmoto Y., Nakamatsu T., Yamashita S., Funahashi T., Matsuzawa Y.;

RA "Adiponectin, an adipocyte-derived plasma protein, inhibits endothelial NF- κ B signaling through a cAMP-dependent pathway.";

RT Circulation 102:1295-1301(2000).

RN [8] FUNCTION.

RX MEDLINE=21372498; PubMed=11479627; DOI=10.1038/90984;

RA Frogiel P., Kadokawa T.;

RA "The fat-derived adiponectin reverses insulin resistance associated with both lipatrophy and obesity.";

RT Nat. Med. 7:941-946(2001).

RN [9] VARIANT ADIPONECTIN DEFICIENCY CYS-112.

RX MEDLINE=20378830; PubMed=10916532;

RA Takahashi M., Arita Y., Yamagata K., Matsukawa Y., Okutomi K., Horie M., Shimomura I., Hotta K., Kuriyama H., Kihara S., Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y.;

RA "Genomic structure and mutations in adipose-specific gene, adiponectin.";

RT Int. J. Obes. Relat. Metab. Disord. 24:861-868(2000).

RN [10] VARIANT ARG-84; MET-117; THR-2164; SER-221 AND PRO-241.

RX MEDLINE=21671103; PubMed=11822766;

RA Hara K., Boutin P., Mori Y., Tobe K., Dina C., Yasuda K., Yamauchi T., Otabe S., Okada T., Eto K., Kadokawa H., Haga R., Akamatsu Y., Nagai R., Yasaki Y., Nagai R., Taniyama M., Matsubara K., Yoda M., Nakano Y., Kimura S., Tomita M., Kimura S., Ito C., Frogiel P., Kadokawa T.;

RA "Genetic variation in the gene encoding adiponectin is associated with an increased risk of type 2 diabetes in the Japanese population.";

RT Diabetes 51:536-540(2002).

CC -!- FUNCTION: Important negative regulator in hematopoiesis and immune systems, may be involved in ending inflammatory responses through its inhibitory functions. Inhibits endothelial NF- κ B.

CC signaling through a cAMP-dependent pathway. Inhibits TNF-alpha-induced expression of endothelial adhesion molecules. Involved in the control of fat metabolism and insulin sensitivity.

CC -!- SUBUNIT: Homooligomer (Potential).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Synthesized exclusively by adipocytes and secreted into plasma.

CC -!- DISEASE: Defects in ACDC are the cause of adiponectin deficiency [IMIM:05441]. The result is a very low concentration of plasma adiponectin. Decreased adiponectin plasma levels are associated with obesity, insulin resistance, and diabetes type 2.

CC -!- PHARMACEUTICAL: Adiponectin might be used in the treatment of diabetes type 2 and insulin resistance.

CC -!- SIMILARITY: Contains 1 CIG domain.

CC -!- SIMILARITY: Contains 1 collagenous domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR D45371; BAA02271;

CC EMBL; AB012165; BAA86716.1; JOINED.

CC EMBL; AB012164; BAA86716.1; JOINED.

CC EMBL; AJ131460; CAB52413.1; JOINED.

CC PIR; JC4708; JC4708.

CC HSSP; Q60594; ICB28.

CC Genew; HGENC:13633; ACDC.

CC MIM; 605441; -.

CC GO; GO:006091; P:energy Pathways; TAS.

CC DR InterPro; IPR001073; CIG helix.

CC DR InterPro; IPR008161; CIG helix.

CC DR InterPro; IPR008160; Collagen.

CC DR InterPro; IPR008983; TNF_like.

CC DR Pfam; PF00386; CIG; 1.

CC DR Pfam; PF01391; Collagen; 1.

CC DR PRINTS; PR00007; COMPLEMENTC1Q.

CC DR PROSITE; PS00007; CIG_helix; 2.

CC DR PROSITE; PS50811; CIG; 1.

CC KW Collagen; Diabetes mellitus; Direct protein sequencing; Disease mutation; Hormone; Hydroxylation; Obesity; Plasma; Polymorphism; Repeat; Signal.

CC PT SIGNAL 1 18

CC PT CHAIN 19 24

CC PT DOMAIN 42 107

CC PT DISUFLID 244

CC PT DOMAIN 108

CC PT DISUFLID 36

CC PT MOD_RES 44

CC PT MOD_RES 47

CC PT MOD_RES 53

CC PT MOD_RES 62

CC PT MOD_RES 71

CC PT MOD_RES 76

CC PT MOD_RES 86

CC PT MOD_RES 95

CC PT MOD_RES 104

CC PT CARBOHYD 230

CC PT VARIANT 84 84

CC PT VARIANT 112 112

CC PT VARIANT 117 117

CC PT VARIANT 164 164

CC PT VARIANT 221 221

CC PT VARIANT 241 241

CC PT SEQUENCE 244 AA; 26414 MW; 648661-204B1018 CRC64;

CC Query Match 100.0%; Score 708; DB 1; Length 244;

CC Best Local Similarity 100.0%; Pred. No. 5.1e-62;

CC Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 FSGVGLETVYVTPNMIRPKFQYQNYQHNGSTGKFCNIPGLYFAVHTVYKDKVKS 60

CC Db 115 FSGVGLETVYVTPNMIRPKFQYQNYQHNGSTGKFCNIPGLYFAVHTVYKDKVKS 174

CC QY 61 LFKKKQKMLTYDQYQENNYDQASGSVVLHLEVGQDQWVQVYGERGRLYADMDNSRF 120

CC Db 175 LFKKKQKMLTYDQYQENNYDQASGSVVLHLEVGQDQWVQVYGERGRLYADMDNSRF 234

CC QY 121 TGFLLIYHTN 130

CC Db 235 TGFLIYHTN 244

RESULT 2	Q95JD7	PRELIMINARY;	PRT;	243 AA.
AC	095JD7;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Adiponectin.			
GN	Name=APM1;			
OC	Macaca mulatta (Rhesus macaque).			
OC	Bukeryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidiae; Cercopithecine; Macaca.			
OC	NCB_TaxID=9544;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Adipose;			
RX	Medline:21232234; PubMed=11334417;			
RA	Hotta K., Funahashi T., Bodkin N.L., Ortmeyer H.K., Arita Y., Hanner B.C., Matsumura Y.;			
RA	"Circulating concentrations of the adipocyte protein adiponectin are decreased in parallel with reduced insulin sensitivity during the progression to type 2 diabetes in rhesus monkeys.";			
RL	Diabetes 50:1126-1133(2001).			
DR	EMBL: AR04407; AAC9202.1; -.			
DR	HSSE; Q60994; I228.			
DR	GO; GO:0005731; C:cytoplasm; IEA.			
DR	InterPro; IPR01073; C1Q.			
DR	InterPro; IPR08161; C1Q helix.			
DR	InterPro; IPR08160; Collagen.			
DR	InterPro; IPR08983; TIN-like.			
DR	Pfam; PF01391; Collagen_1.			
DR	PRINTS; PR00007; COMPLEMENTC1Q.			
DR	PRODOM; PD00007; C1Q helix; 1.			
DR	SMART; SN00110; C1Q; 1.			
KW	PROSITE; PS01113; C1Q; 1.			
KW	Collagen.			
SQ	SEQUENCE 243 AA; 26264 MW; 49445DAP2B4613FD CRC64;			
Query Match	99.9%; Score 707; DB 2; Length 243;			
Best Local Similarity	99.2%; Pred. No. 6.4e-62;			
Matches	129; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
QY	1 FSVGLEYTVTIPNNPIRFKTFPKFVNQHNDGTSKFKHCNIPGLYFAYHITVNMKVKS			
Db	115 FSVGLEYTVTIPNNPIRFKTFPKFVNQHNDGTSKFKHCNIPGLYFAYHITVNMKVKS			
QY	61 LFKKDKAMLFYDQYQENNNDQASGVVLHLVEQDQVWILQVYGERGERNLQYADNDSTP			
Db	175 LFKKDKAMLFYDQYQENNNDQASGVVLHLVEQDQVWILQVYGERGERNLQYADNDSTP			
QY	121 TGFELLYHDTN 130			
Db	235 TGFELLYHDTN 244			
RESULT 4	APML_MOUSE	STANDARD;	PRT;	247 AA.
ID	APML_MOUSE			
AC	Q60994; Q62400; Q9DC68;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DB	Adiponectin precursor (Adipocyte, C1q and collagen domain containing protein) (30 kDa adipocyte complement-related protein) (ACRP30)			
DE	(Adipocyte Specific protein AdipoQ).			
GN	Name=Adcc; Synonyms=Acrp30, AdipoQ, Apm1;			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OC	NCB_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Adipocyte;			
RX	Medline:96070757; PubMed=7592907; DOI=10.1074/jbc.270.45.26746;			
RA	Scherer P.E., Williams S., Fogliano M., Baldini G., Lodish H.F.:			
RT	"A novel serum protein similar to C1q, produced exclusively in adipocytes."			
RL	J. Biol. Chem. 270:26746-26749(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fibroblast;			
RX	Medline:96070999; PubMed=8631877; DOI=10.1074/jbc.271.18.10697;			
RA	Hu E., Liang P., Spiegelman B.M.:			
RT	"AdipoQ is a novel adipose-specific gene dysregulated in obesity."			
RL	J. Biol. Chem. 271:10697-10703(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	Pubmed:1165643; DOI=10.1006/bbrc.2001.4217;			
RA	Dab K., Lin Y., Widen E., Zhang Y., Scherer P.E.;			
RT	"Chromosomal localization, expression pattern, and promoter analysis of the mouse gene encoding adipocyte-specific secretory protein Acrp30."			
RT				

DR	InterPro; IPR008161; Clg helix.
DR	InterPro; IPR008160; Collagen.
DR	InterPro; IPR008983; TNF_like.
DR	Pfam; PF00386; Clq; 1.
DR	Pfam; PF01391; Collagen; 1.
DR	PRINTS; PR00007; COMPLEMNTC1Q.
DR	ProDom; PRO00007; Clq helix; 1.
DR	SMART; SM00110; Clq; 1.
DR	PROSITE; PS01113; Clq; 1.
KW	Collagen.
SEQUENCE	247 AA; 26751 MW; 0D3FA64C789CAEF3 CRC64;
RN	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RC	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/3505555001;
RC	RIKEN FANTOM Consortium;
RC	"Functional annotation of a full-length mouse cDNA collection.";
RC	Nature 409:685-690(2001).
RP	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RP	The FANTOM Consortium;
RP	the RIKEN Genome Exploration Research Group Phase I & II Team;
RP	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length DNAs.";
RN	Nature 420:563-573(2002).
[4]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RP	MEDLINE=20459374; PubMed=11042159; DOI=10.1101/gr.145100;
RA	Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.;
RA	Kondo H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RT	Genome Res. 10:1617-1630(2000).
[5]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RP	MEDLINE=20509133; PubMed=11076861; DOI=10.1101/gr.152600;
RA	Shibata K.; Itoh M.; Aizawa K.; Nagao S.; Sasaki N.; Carninci P.;
RA	Kondo H.; Akiyama J.; Nishi K.; Kitisuna T.; Tashiro H.; Itoh M.;
RA	Sumi N.; Ishii Y.; Nakamura S.; Hazzama M.; Nishine T.; Harada A.;
RA	Yamamoto R.; Matsubumi H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.;
RA	Fujiwaka S.; Inoue K.; Togawa Y.; Iizawa M.; Ohara E.; Wachikita M.;
RA	Yoneda Y.; Ishikawa T.; Ozawa K.; Tanka T.; Matsura S.; Kawai J.;
RA	Okazaki Y.; Muramatsu M.; Inoue Y.; Kira A.; Hayashizaki Y.;
RT	"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
RT	Genome Res. 10:1757-1771(2000).
[6]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA	Adachi J.; Aizawa K.; Akimura T.; Arakawa T.; Bono H.; Carninci P.;
RA	Fukuda S.; Furuno M.; Hanagaki T.; Hara A.; Hashizume W.;
RA	Hayashida K.; Hayatsu N.; Hiramoto K.; Hirokawa T.; Hirozane T.;
RA	Kotoh F.; Imotani K.; Ishii Y.; Itoh M.; Kagawa T.; Kasukawa T.;
RA	Kurohata C.; Matsuyama T.; Miyazaki A.; Murata M.; Nakamura M.;
RA	Nishi K.; Nomura K.; Numazaki R.; Ohno M.; Ohbato N.; Okazaki Y.;
RA	Saito R.; Saitoh H.; Sakai C.; Sakai K.; Sakazume N.; Sano H.;
RA	Sasaki D.; Shibata K.; Shingawa A.; Shiraki T.; Sogabe Y.; Tadami M.;
RA	Tagawa A.; Takahashi F.; Takaku-Akabira S.; Takeda Y.; Tanaka T.;
RA	Tomaru A.; Toyai T.; Yasunishi A.; Muramatsu M.; Hayashizaki Y.;
RA	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AK041214; BAC3.0866.1; -.
DR	HSPP; Q50994; 1C28.
DR	MGI; 106675; Accd.
DR	GO; GO:0005615; C: extracellular space; TAS.
DR	GO; GO:0005179; F: hormone activity; TAS.
DR	GO; GO:0005515; F: protein binding; IPI.
DR	GO; GO:0006635; P: fatty acid beta-oxidation; IMP.
DR	GO; GO:0006006; P: glucose metabolism; IDA.
DR	InterPro; IPR001073; Clq.
QY	Query Match 1 FSGVGLTYVTPNMPRTFKFVYDQHNGSTGKPHCNPGGLYVAYHITVYMKVKVS 89.4%; Score 633; DB 2; Length 244; Best Local Similarity 86.9%; Pred. No. 1.4e-54; Matches 113; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
Db	115 FSGVGLTYVTPNMPRTFKFVYDQHNGSTGKPHCNPGGLYVAYHITVYMKVKVS 60 FSGVGLTYVTPNMPRTFKFVYDQHNGSTGKPHCNPGGLYVAYHITVYMKVKVS 174
Qy	61 LFKKOKAMLFITDQYQENNTDQASSVLLHVGQWMLQYEGEGRNLGYADNDIDSTP 120

DR	PROSITE; PS0113; C1Q; 1.	KW	Collagen.
KW	Collagen.	SQ	SEQUENCE
FT	NON-TER	1	1
FT	NON-TER	194	194
SQ	SEQUENCE	194 AA;	20890 MW;
Query	Match	72.6%	Score 514; DB 2; Length 194;
	Best Local Similarity	89.3%	Pred. No. 6. 8e-43;
	Matches	92	Mismatches 3; Indels 0; Gaps 0;
Qy	1	FSVGLGETTYVTPNMPTRFTKIFYNQHQHYDSTGKPHCNTRGLYFAVHITVYMKDVKS	60
Db	92	FSVGLGETTYVTPNMPTRFTKIFYNQHQHYDSTGKPHCNTRGLYFAVHITVYMKDVKS	151
Qy	61	LFKKDKAMFLYDQOQENNTDQASGSVVLHLEVGDOWLQYLG	103
Db	152	LFKKDKAMFLYDQOQENNTDQASGSVVLHLEVGDOWLQYLG	194
RESULT	13		
R6D445	PRELIMINARY;	PRT;	235 AA.
ID	Q6DD45		
AC	Q6DD45;		
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)	DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE	Col1a1-prov protein.	DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
GN	Name=col1a1-prov;	DB	MGC44292 protein.
OS	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)	GN	Name=MGC44292;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OS	Xenopus laevis (African clawed frog).
OC	Xenopoda; Xenopus.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OX	NCBI_TaxID=8364;	OC	Xenopoda; Xenopus.
RN	[1]	NCBI_TaxID=8355;	OX
RP	SEQUENCE FROM N.A.	RN	
RX	TISSUE=Whole body;	RX	
RA	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	RA	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	RA	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	RA	
RA	Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	RA	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	RA	
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	RA	
RA	Stapleton M., Soares M.B., Bandal M.F., Casavant T.L., Scheetz T.E.,	RA	
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,	RA	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,	RA	
RA	Bosak S.A., McEwan J.R., McEwan K.J., Malek J.A., Gunaratne P.H.,	RA	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	RA	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	RA	
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,	RA	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	RA	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	RA	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	RA	
RA	Krzywinski M.I., Skalska U., Smalius D.E., Scherich A., Schein J.E.,	RA	
RA	Jones S.J., Marra M.A.,	RA	
RT	"Generation and initial analysis of more than 15,000 full-length human	RA	
RT	and mouse cDNA sequences,"	RA	
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RA	
RN	[2]	RA	
RP	SEQUENCE FROM N.A.	RN	
RC	TISSUE=Whole body;	RC	
RA	Klein S., Gerhard D.S.;	RC	
RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	RC	
RA	EMBL; BC05339; AAH5339_1; -.	RC	
DR	GO; GO:0005737; C:cytoplasm; IEA.	RC	
DR	GO; GO:0006817; R:phosphate transport; IEA.	RC	
DR	InterPro; IPR01073; C1Q.	RC	
DR	InterPro; IPR008160; Collagen.	RC	
DR	InterPro; IPR008983; TNF_like.	RC	
DR	Pfam; PF00386; C1Q; 1.	RC	
DR	Pfam; PF01391; Collagen; 1.	RC	
DR	PRINTS; PR0007; COMPLEMTC1Q.	RC	
DR	SMART; SM00110; C1Q; 1.	RC	
DR	PROSITE; PS0113; C1Q; 1.	RC	
RESULT	14		
R6D445	PRELIMINARY;	PRT;	235 AA.
ID	Q6GLS9		
AC	Q6GLS9;		
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE	MGC44292 protein.	DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
GN	Name=MGC44292;	DB	MGC44292 protein.
OS	Xenopus laevis (African clawed frog).	GN	Name=MGC44292;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	OS	Xenopus laevis (African clawed frog).
OC	Xenopoda; Xenopus.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OX	NCBI_TaxID=8355;	OC	Xenopoda; Xenopus.
RN	[1]	NCBI_TaxID=8355;	OX
RP	SEQUENCE FROM N.A.	RN	
RX	TISSUE=Brain;	RX	
RA	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	RA	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	RA	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	RA	
RA	Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	RA	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	RA	
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	RA	
RA	Stapleton M., Soares M.B., Bandal M.F., Casavant T.L., Scheetz T.E.,	RA	
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,	RA	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,	RA	
RA	Bosak S.A., McEwan J.R., McEwan K.J., Malek J.A., Gunaratne P.H.,	RA	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	RA	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	RA	
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,	RA	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	RA	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	RA	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	RA	
RA	Krzywinski M.I., Skalska U., Smalius D.E., Scherich A., Schein J.E.,	RA	
RA	Jones S.J., Marra M.A.,	RA	
RT	"Generation and initial analysis of more than 15,000 full-length human	RA	
RT	and mouse cDNA sequences,"	RA	
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RA	
RN	[2]	RA	
RP	SEQUENCE FROM N.A.	RN	
RC	TISSUE=Brain;	RC	
RA	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;	RA	
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,	RA	
RA	Richardson P.,	RA	
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus	RT	
RT	initiative,"	RT	
RT	Dev. Dyn. 225:384-391 (2002).	RT	
RL	[3]	RT	
RP	SEQUENCE FROM N.A.	RL	
RC	TISSUE=Brain;	RC	
RA	Klein S., Gerhard D.S.,	RC	
RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	RC	
RA	EMBL; BC074375; AAH74375_1; -.	RC	

DR GO; GO:0005373; C:cytoplasm; IEA.
 DR GO; GO:0006817; P:phosphate transport; IEA.
 DR InterPro; IPR01073; C1Q.
 DR InterPro; IPR08160; Collagen.
 DR InterPro; IPR08183; TNF-like.
 DR Pfam; PFO0386; C1Q; 1.
 DR Pfam; PRO1391; Collagen; 1.
 DR PRINTS; PRO0007; COMPLEMENTC1Q.
 DR SMART; SM00110; C1Q; 1.
 DR PROSITE; PS01113; C1Q; 1.
 KW Collagen.
 SQ Sequence 235 AA; 25708 MW; 7B5E24A4BE0DBD98 CRC64;
 Query Match 67.5%; Score 478; DB 2; Length 235;
 Best Local Similarity 65.6%; Score 3.1e-39;
 Matches 84; Conservative 22; Mismatches 22; Indels 0; Gaps 0;
 Matches 84; Conservative 22; Mismatches 22; Indels 0; Gaps 0;
 Qy 1 FSVGLETYVTLIPNMPRFKIFVQNYHGDGSTGKFCHNIPGLYYFAYHITVYMKDVKS 60
 Db 108 FSWGLISTKESLPRNPVIRPFTKVFNEQRHYDESTGFKRSAIKGLYQFSYHLLTVYMKDVKG 167
 Qy 61 LFKKDKAMLFITYPOYQENNNDQASGSVVLHLEFGDQWILQVIGEGERGNGLYADNDNDSTF 120
 Db 168 LYRNNKPMTFDQFQSNNDQASGSVVLQLEVGDIEINLQIVGDESFSGIYGDNLNDSTP 227
 Qy 121 TGFLLYHD 128
 Db 228 SGILLYPD 235

This Page Blank (uspto)